



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 160284

TO: Patricia Duffy
Location: REM-3B05/3C18
Art Unit: 1645
Thursday, July 28, 2005

Case Serial Number: 09/900766

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: 571-272-2527

Paul.schulwitz@uspto.gov

Search Notes

Examiner Duffy,

Please review the attached search results.

If you have any questions or if you would like to refine the search query, please feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
REM-1A65
571-272-2527



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160284

From: Duffy, Patricia
Sent: Friday, July 22, 2005 6:51 PM
To: STIC-Biotech/ChemLib
Subject: sequence search 09/900,766

Importance: High

In RE: 09/900,766

Please search SEQ ID NO:7 in commercial and interference databases.
Please print out top 100 hits in each category.

Thanks mucho.

Patricia A. Duffy, Ph.D.
Art Unit 1645
Remsen 3B05; Mailbox 3C18
571-272-0855

STAFF USE ONLY

Searcher: _____
 Searcher Phone: 2-_____
 Date Searcher Picked up: _____
 Date Completed: 7/18
 Searcher Prep/Rev. Time: _____
 Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 11:08:35 ; Search time 159 Seconds
(without alignments)
570.033 Million cell updates/sec

Title: US-09-900-766-7

Perfect score: 1238

Sequence: 1 SEKSEEINEKDLRKSELR.....RDNKTINSENLHLYLTYT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database :

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1238	100.0	233	10	US-09-900-766-7
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3	1238	100.0	257	15	US-10-267-682-112
4	1238	100.0	257	15	US-10-267-748-112
5	1238	100.0	257	16	US-10-428-817A-188
6	1230	97.7	233	10	US-09-900-766-3
7	1188	96.0	248	9	US-09-870-759-16
8	1188	96.0	248	10	US-09-751-708A-16
9	1188	96.0	248	16	US-10-428-817A-12
10	1188	96.0	248	17	US-10-937-758A-16
11	1107	89.4	233	10	US-09-900-766-2
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					Sequence 8, Appli
					Sequence 112, App
					Sequence 112, App
					Sequence 188, App
					Sequence 3, Appli
					Sequence 16, Appl
					Sequence 16, Appl
					Sequence 12, Appl
					Sequence 16, Appl
					Sequence 2, Appli

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1023	82.6	233	14	US-10-283-838-7	Sequence 7, Appli
1023	82.6	257	15	US-10-267-682-113	Sequence 113, App
1023	82.6	257	15	US-10-267-748-113	Sequence 113, App
1019	82.3	233	15	US-10-354-948-4	Sequence 4, Appli
1013	81.8	257	9	US-09-870-759-8	Sequence 8, Appli
1013	81.8	257	10	US-09-751-708A-8	Sequence 8, Appli
1013	81.8	257	16	US-10-428-817A-4	Sequence 4, Appli
1013	81.8	257	17	US-10-937-758A-8	Sequence 8, Appli
1000	80.8	257	14	US-10-002-784A-2	Sequence 2, Appli
1000	80.8	257	17	US-10-767-687-2	Sequence 2, Appli
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ALIGNMENTS

RESULT 1

US-09-900-766-7
; Sequence 7, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US010104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-7

Query Match 100.0%; Score 1238; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 6.7e-105;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 SEKSEINEKDLRKSELOLNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFTG 60
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYOCAGTGNKTACMYGGVTLHDNNRLT 120
Db 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYOCAGTGNKTACMYGGVTLHDNNRLT 120
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QY 121 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 121 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGPDTLLRIYRDNKTINSENHLIDLTYTT 233
Db 181 RGLIVFHSSEGSTVSVDLFDAGQGPDTLLRIYRDNKTINSENHLIDLTYTT 233

RESULT 2

US-10-283-838-8
; Sequence 8, Application US/10283838
; Publication No. US20030092894A1
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; Johan Hansson, Terje Kalland, Lars
; Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,838
; FILING DATE: 30-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,692
; FILING DATE: August 12, 1996
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-283-838-8

Query Match 100.0%; Score 1238; DB 14; Length 233;
Best Local Similarity 100.0%; Pred. No. 6.7e-105;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOLNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFTG 60
Db 1 SEKSEINEKDLRKSELOLNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFTG 60

QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYOCAGTGNKTACMYGGVTLHDNNRLT 120
Db 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYOCAGTGNKTACMYGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 121 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGPDTLLRIYRDNKTINSENHLIDLTYTT 233
Db 181 RGLIVFHSSEGSTVSVDLFDAGQGPDTLLRIYRDNKTINSENHLIDLTYTT 233

RESULT 3

US-10-267-682-112
; Sequence 112, Application US/10267682
; Publication No. US2004003235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-267-682-112

Query Match 100.0%; Score 1238; DB 15; Length 257;
Best Local Similarity 100.0%; Pred. No. 7.6e-105;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOLNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFTG 60
Db 25 SEKSEINEKDLRKSELOLNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFTG 84

QY	61	HPWYNDDLVLDSKDATNKYGKKVDLYGAYGYQCAGGTPTNTACMYGGVTLHDNNRLT	120
Dd	85	HPWYNDDLVLDSKDATNKYGKKVDLYGAYGYQCAGGTPTNTACMYGGVTLHDNNRLT	144
QY	121	EKKVPINLWIDCKTTVPIDKVKTSKEVTVQELDLOARHYLGKFGLNSDSFGSKVQ	180
Dd	145	EKKVPINLWIDCKTTVPIDKVKTSKEVTVQELDLOARHYLGKFGLNSDSFGSKVQ	204
QY	181	RGLIVPHSSEGSTVSYDLFDAQQGPDTLLRIYRDNKTINSENHLIDLTYTT	233
Dd	205	RGLIVPHSSEGSTVSYDLFDAQQGPDTLLRIYRDNKTINSENHLIDLTYTT	257

```

RESULT 4
US-10-267-748-112
; Sequence 112, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
;
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
;
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
;
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
;

```

```

NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/267,748
  FILING DATE: 08-Oct-2002
  CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/08/484,223A
    FILING DATE: 07-JUN-1995
    ATTORNEY/AGENT INFORMATION:
      NAME: Coruzzi, Laura A.
      REGISTRATION NUMBER: 30,742
      REFERENCE/DOCKET NUMBER: 7872-029
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: (212) 790-9090
        TELEFAX: (212) 869-9741/8864
        TELEX: 66141 PENNIE
      INFORMATION FOR SEQ ID NO: 112:
        SEQUENCE CHARACTERISTICS:
          LENGTH: 257 amino acids
          TYPE: amino acid
          STRANDEDNESS: <Unknown>
          TOPOLOGY: unknown
        MOLECULE TYPE: protein
        SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-267-748-112

```

```

Query Match      100.0%; Score 1238; DB 15; Length 257;
Best Local Similarity 100.0%; Pred. No. 7 6e-105;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEETNEKDLRKKSLEQRNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTTG 60

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Db	25	SEKSEEEINEKDLRKSKSLQNALSNLRQIYYINEKAITENKESDDQFLENTLLFKGFPFG	84
Qy	61	HPWYNDDLVLGSKDANTKYGKKVDLYGAYYG*QCAGGTPNKTACMYGGVTLHDNNRLT	120
Db	85	HPWYNDDLVLGSKDANTKYGKKVDLYGAYYG*QCAGGTPNKTACMYGGVTLHDNNRLT	144
Qy	121	EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQBELDQARHYLHGKFGLYNSDSFGGKVQ	180
Db	145	EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQBELDQARHYLHGKFGLYNSDSFGGKVQ	204
Qy	181	RGILVFHSSSGSTVSYDLFDAQQGYPTTLRIYRDNKTTINSENGLHIDLYLYTT	233
Db	205	RGILVFHSSSGSTVSYDLFDAQQGYPTTLRIYRDNKTTINSENGLHIDLYLYTT	257

```

RESULT 5
US-10-428-817A-188
; Sequence 188, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 188
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-188

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	Query Match	100.0%;	Score 1238;	DB 16;	Length 257;
	Best Local Similarity	100.0%;	Pred. No. 7.6e-105;		
	Matches 233;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	SEKSEINEKDLRKKSELQRLNALSNLRQIYYINEKAITENKESDDQFLENTLLFKGPFPTG	60		
Db	25	SEKSEINEKDLRKKSELQRLNALSNLRQIYYINEKAITENKESDDQFLENTLLFKGPFPTG	84		
Qy	61	HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDHNNRLT	120		
Db	85	HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDHNNRLT	144		
Qy	121	EEEKVPINLWIDGKQTTPVDKVKTSKKEVTVQBELDQARHYLHGKFGLYNSDSFGGKVQ	180		
Db	145	EEEKVPINLWIDGKQTTPVDKVKTSKKEVTVQBELDQARHYLHGKFGLYNSDSFGGKVQ	204		
Qy	181	RGILVPHSSSEGSTVSYDLFDQAQGYPTTLRLIYRDNKTINSENLHIDLILYTTT	233		
Db	205	RGILVPHSSSEGSTVSYDLFDQAQGYPTTLRLIYRDNKTINSENLHIDLILYTTT	257		

RESULT 6
US-09-090-766-3
; Sequence 3, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:

APPLICANT: FORSBERG, GORAN
APPLICANT: ERLANDSSON, EVA
APPLICANT: ANTONSSON, PER
APPLICANT: WALSE, BJORN
TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
FILE REFERENCE: P02188US0.10104199
CURRENT APPLICATION NUMBER: US/09/900,766
CURRENT FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 233
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: peptide
LOCATION: (1)..(233)
OTHER INFORMATION: Chimeric Protein
US-09-900-766-3

Query Match 97.7%; Score 1210; DB 10; Length 233;
Best Local Similarity 97.9%; Pred. No. 2.4e-102;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Qy 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Qy 181 RGLIVFHSSEGSTSVSYDLFDAQGYPTDLLRIYRDNKNTINSENHLIDLYTT 233
Db 181 RGLIVFHSSEGSTSVSYDLFDAQGYPTDLLRIYRDNKNTINSENHLIDLYTT 233

RESULT 7
US-09-870-759-16
Sequence 16, Application US/09870759
Patent No. US20020177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 248
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-870-759-16

Query Match 96.0%; Score 1188; DB 9; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.7e-100; Indels 0; Gaps 0;
Matches 224; Conservative 0; Mismatches 0;

Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
Qy 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
Qy 181 RGLIVFHSSEGSTSVSYDLFDAQGYPTDLLRIYRDNKNTINSEN 224
Db 205 RGLIVFHSSEGSTSVSYDLFDAQGYPTDLLRIYRDNKNTINSEN 248

RESULT 8
US-09-751-708A-16
Sequence 16, Application US/09751708A
Publication No. US20030157113A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 751708
CURRENT APPLICATION NUMBER: US/09/751,708A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 60/173,371
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 248
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-751-708A-16

Query Match 96.0%; Score 1188; DB 10; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.7e-100; Indels 0; Gaps 0;
Matches 224; Conservative 0; Mismatches 0;

Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
Qy 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
Qy 181 RGLIVFHSSEGSTSVSYDLFDAQGYPTDLLRIYRDNKNTINSEN 224
Db 205 RGLIVFHSSEGSTSVSYDLFDAQGYPTDLLRIYRDNKNTINSEN 248

RESULT 9
US-10-428-817A-12
Sequence 12, Application US/10428817A
Publication No. US20040214783A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 38373-189118
CURRENT APPLICATION NUMBER: US/10/428,817A
CURRENT FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: US 60/378,988
PRIOR FILING DATE: 2002-05-08
PRIOR APPLICATION NUMBER: US 60/389,366
PRIOR FILING DATE: 2002-06-15
PRIOR APPLICATION NUMBER: US 60/406,697
PRIOR FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: US 60/406,750
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/415,310
PRIOR FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US 60/415,400
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: US 60/438,686

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; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-12

Query Match      96.0%; Score 1188; DB 16; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.7e-100; Indels 0; Gaps 0;
Matches 224; Conservative 0; Mismatches 0;

Qy 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYYNKAITENKESDDQFLENTLLFKGFPTG 60
Db 25 SEKSEINEKDLRKKSSELQNALSNLRQIYYYNKAITENKESDDQFLENTLLFKGFPTG 84

Qy 61 HPWYNDLLVLDLGSKDATNKYKGVLDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVLDLGSKDATNKYKGVLDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLT 144

Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204

Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSEN 224
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSEN 248

RESULT 10
US-10-937-758A-16
; Sequence 16, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-937-758A-16

Query Match      96.0%; Score 1188; DB 17; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.7e-100; Indels 0; Gaps 0;
Matches 224; Conservative 0; Mismatches 0;

Qy 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYYNKAITENKESDDQFLENTLLFKGFPTG 60
Db 25 SEKSEINEKDLRKKSSELQNALSNLRQIYYYNKAITENKESDDQFLENTLLFKGFPTG 84

Qy 61 HPWYNDLLVLDLGSKDATNKYKGVLDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVLDLGSKDATNKYKGVLDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLT 144

Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204

Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSEN 224
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSEN 248

RESULT 11
US-09-900-766-2
```

```
; Sequence 2, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERNANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(233)
; OTHER INFORMATION: Chimeric Protein
US-09-900-766-2

Query Match      89.4%; Score 1107; DB 10; Length 233;
Best Local Similarity 89.7%; Pred. No. 6.4e-93;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYYNKAITENKESDDQFLENTLLFKGFPTG 60
Db 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYYNKAITENKESDDQFLENTLLFKGFPTG 60

Qy 61 HPWYNDLLVLDLGSKDATNKYKGVLDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLT 120
Db 61 HPWYNDLLVLDLGSSTAATSEYEGSSVDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLT 120

Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180

Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHLIDLYLTT 233
Db 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTISLSISLYLTT 233

RESULT 12
US-09-900-766-1
; Sequence 1, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERNANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(672)
; OTHER INFORMATION: Conjugate protein
US-09-900-766-1

Query Match      89.4%; Score 1107; DB 10; Length 672;
Best Local Similarity 89.7%; Pred. No. 2.6e-92;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
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QY 1 SEKSEINEKDLRKSELOALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
DB 236 SEKSEINEKDLRKSELOALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFFTG 285
QY 61 HPWYNDLLVLDGSKDANKYKGGKVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLT 120
DB 286 HPWYNDLLVLDGSKDANKYKGGKVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLT 345
QY 121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 346 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDILLRIYRDNKTINSENHLDLYTT 233
DB 406 RGLIVFHSSEGSTVSVDLFDAGQYPTDILLRIYRDNKTINSENHLDLYTT 458

RESULT 13
US-09-900-766-4
; Sequence 4, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US010104139
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-4

Query Match 82.6%; Score 1023; DB 10; Length 233;
Best Local Similarity 82.0%; Pred. No. 3.1e-85;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
QY 61 HPWYNDLLVLDGSKDANKYKGGKVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLT 120
DB 61 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLT 120
QY 121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDILLRIYRDNKTINSENHLDLYTT 233
DB 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDILLRIYRDNKTINSENHLDLYTT 233

RESULT 14
US-10-283-838-7
; Sequence 7, Application US/10283838
; Publication No. US2003002894A1
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlstén,
; Johan Hansson, Terje Kalland, Lars
; Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor

CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,838
FILING DATE: 30-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/695,692
FILING DATE: August 12, 1996
APPLICATION NUMBER: 9601245-5
FILING DATE: March 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Krieger, Paul E.
REGISTRATION NUMBER: 25,886
REFERENCE/DOCKET NUMBER: 41986/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-283-838-7

Query Match 82.6%; Score 1023; DB 14; Length 233;
Best Local Similarity 82.0%; Pred. No. 3.1e-85;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
QY 61 HPWYNDLLVLDGSKDANKYKGGKVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLT 120
DB 61 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLT 120
QY 121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDILLRIYRDNKTINSENHLDLYTT 233
DB 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDILLRIYRDNKTINSENHLDLYTT 233

RESULT 15
US-10-267-682-113
; Sequence 113, Application US/10267682
; Publication No. US2004003325A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-267-682-113

Query Match 82.6%; Score 1023; DB 15; Length 257;
Best Local Similarity 82.0%; Pred. No. 3.5e-85;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNKAITENKESDDOFLNTLLKGFPTG 60
Db 25 SEKSEINEKDLRKKSSELQALGNLQIYYNKAITENKESHDDQFLQHTILFKGFPTD 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVK 180
Db 145 BEKKVPINLWIDGKQNTVPLETVTNKKNVTQVQLDLQARRYLOEKYNLYNSDVFDGKVK 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHLDLYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGYQNTLLRIYRDNKTINSENHLDLYLTS 257

RESULT 16
US-10-267-748-113
Sequence 113, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-267-748-113

Query Match 82.6%; Score 1023; DB 15; Length 257;
Best Local Similarity 82.0%; Pred. No. 3.5e-85;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNKAITENKESDDOFLNTLLKGFPTG 60
Db 25 SEKSEINEKDLRKKSSELQALGNLQIYYNKAITENKESHDDQFLQHTILFKGFPTD 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVK 180
Db 145 BEKKVPINLWIDGKQNTVPLETVTNKKNVTQVQLDLQARRYLOEKYNLYNSDVFDGKVK 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHLDLYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGYQNTLLRIYRDNKTINSENHLDLYLTS 257

RESULT 17
US-10-354-948-4
Sequence 4, Application US/10354948
Publication No. US20030202962A1
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
Elmslie, Robyn E.
Potter, Terence A.
TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.

ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/10/354,948
APPLICATION NUMBER: US/10/354,948
FILING DATE: 29-Jan-2003
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/580,806
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-354-948-4

Query Match 82.3%; Score 1019; DB 15; Length 233;
Best Local Similarity 81.9%; Pred. No. 7.1e-85;
Matches 190; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 2 EKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 61
DB 2 EKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 61
QY 62 PWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQR 181
DB 122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQR 181
QY 182 GLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLDLYLYTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAQGSNTLLRIYRDNKTINSENHLDLYLYTS 233

RESULT 18
US-09-870-759-8
; Sequence 8, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-8

Query Match 81.8%; Score 1013; DB 9; Length 257;
Best Local Similarity 81.5%; Pred. No. 2.9e-84;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
QY 61 HPYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQR 180
DB 145 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQR 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGSNTLLRIYRDNKTINSENHLDLYLYTS 257

RESULT 19
US-09-751-708A-8
; Sequence 8, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-8

Query Match 81.8%; Score 1013; DB 10; Length 257;
Best Local Similarity 81.5%; Pred. No. 2.9e-84;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
QY 61 HPYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQR 180
DB 145 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQR 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGSNTLLRIYRDNKTINSENHLDLYLYTS 257

RESULT 20
US-10-428-817A-4
; Sequence 4, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15

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; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 4
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-4

Query Match      81.8%; Score 1013; DB 16; Length 257;
Best Local Similarity 81.5%; Pred. No. 2,9e-84;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKXSELQNALNLROIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKXSELQNALNLROIYYNEKAITENKESHQFLQHTILFKGFFTN 84
Qy 61 HPWYNDLLVLDGSKDATNKYKGVVLYGAYGYOCAGTGNKTCACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVKYKGVVLYGAYGYOCAGTGNKTCACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTPLETVTNKKNVTVQELDLQARHYLQEKYLYNSDVFDGKVQ 204
Qy 181 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHIDILYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQQGQVSNLTLRIYRDNKTINSENHIDILYLYTS 257

RESULT 21
US-10-937-758A-8
; Sequence 8, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-937-758A-8

Query Match      81.8%; Score 1013; DB 17; Length 257;
Best Local Similarity 81.5%; Pred. No. 2,9e-84;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKXSELQNALNLROIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKXSELQNALNLROIYYNEKAITENKESHQFLQHTILFKGFFTN 84
Qy 61 HPWYNDLLVLDGSKDATNKYKGVVLYGAYGYOCAGTGNKTCACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVKYKGVVLYGAYGYOCAGTGNKTCACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
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Db 145 EEKVPINLWIDGKQTTPLETVTNKKNVTVQELDLQARHYLQEKYLYNSDVFDGKVQ 204
Qy 181 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHIDILYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQQGQVSNLTLRIYRDNKTINSENHIDILYLYTS 257

RESULT 22
US-10-002-784A-2
; Sequence 2, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURES:
; OTHER INFORMATION: mutant staphylococcal enterotoxin A periplasmic
US-10-002-784A-2

Query Match      80.8%; Score 1000; DB 14; Length 257;
Best Local Similarity 80.7%; Pred. No. 4,4e-83;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKXSELQNALNLROIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKXSELQNALNLROIYYNEKAITENKESHQFLQHTILFKGFFTD 84
Qy 61 HPWYNDLLVLDGSKDATNKYKGVVLYGAYGYOCAGTGNKTCACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVKYKGVVLYGAYGYOCAGTGNKTCACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTPLETVTNKKNVTVQELDLQARHYLQEKYLYNSDVFDGKVQ 204
Qy 181 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHIDILYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQQGQVSNLTLRIYRDNKTINSENHIDILYLYTS 257

RESULT 23
US-10-767-687-2
; Sequence 2, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavarl
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MPMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
```

SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/767,687
FILING DATE: 29-Jan-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 257
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-767-687-2

Query Match 80.8%; Score 1000; DB 17; Length 257;
Best Local Similarity 80.7%; Pred. No. 4.4e-83;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKESELQNALSNLRQIYYNEKAITENKESDDOQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKESELQNALSNLRQIYYNEKAITENKESDDOQFLENTLLFKGFFTD 84
QY 61 HSWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVRFDSKDQIVDKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EKKVPINLWLDGKQNTVPLETVTKNKNVTQELDLQARRYLQEKYNLYNSDVFQGVQ 204
QY 181 RGLVPHSSEGSTVSYDLFDAQGYPDTLRLRYRNKNTINSENHLHDLYLTT 233
DB 205 RGLVPHSTEPSVNYDLFQAQGYNSNTLLRIRYRNKNTINSENMHDIYLYTS 257

RESULT 24
US-10-002-784A-4
Sequence 4, Application US/10002784A
Publication No. US20030036644A1
GENERAL INFORMATION:
/33
APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Word 6.0
SEQ ID NO 4
LENGTH: 233
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: mutant staphylococcal enterotoxin A cytoplasmic
US-10-002-784A-4

Query Match 80.5%; Score 996; DB 14; Length 233;
Best Local Similarity 80.6%; Pred. No. 9.1e-83;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKKESELQNALSNLRQIYYNEKAITENKESDDOQFLENTLLFKGFFTGH 61
DB 2 EKSEINEKDLRKKESELQNALSNLRQIYYNEKAITENKESDDOQFROHTILFKGFFTGH 61
QY 62 PWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVRFDSKDQIVDKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 181
DB 122 EKKVPINLWLDGKQNTVPLETVTKNKNVTQELDLQARRYLQEKYNLYNSDVFQGVQ 181
QY 182 GLIVPHSSEGSTVSYDLFDAQGYPDTLRLRYRNKNTINSENHLHDLYLTT 233
DB 182 GLIVPHSTEPSVNYDLFQAQGYNSNTLLRIRYRNKNTINSENMHDIYLYTS 233

RESULT 25
US-10-767-687-4
Sequence 4, Application US/10767687
Publication No. US20050064526A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent At
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/767,687
FILING DATE: 29-Jan-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-7714
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 233
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-767-687-4

Query Match 80.5%; Score 996; DB 17; Length 233;
Best Local Similarity 80.6%; Pred. No. 9.1e-83;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKKESELQNALSNLRQIYYNEKAITENKESDDOQFLENTLLFKGFFTGH 61
DB 2 EKSEINEKDLRKKESELQNALSNLRQIYYNEKAITENKESDDOQFROHTILFKGFFTGH 61
QY 62 PWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLTE 121

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Db 62 SWYNDLLVRPDSKOTVDYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLTE 121
Qy 122 EKKVPINLWIDGKOTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVOR 181
Db 122 EKKVPINLWIDGKQNTVPLETVKTKNGVTVQELDLQARRYLQEKYLNYSNVDVDFGKVOR 181
Qy 182 GLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSNLHIDLTYTT 233
Db 182 GLIVFHTSTSPSVNYDLFGAQQYSNTLLRIYRDNKTINSNMHIDIYLYTS 233

RESULT 26
US-10-428-817A-182
; Sequence 182, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 182
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-182

Query Match 80.0%; Score 991; DB 16; Length 231;
Best Local Similarity 80.3%; Pred. No. 2,6e-82;
Matches 187; Conservative 18; Mismatches 26; Indels 2; Gaps 1;

Qy 1 SEKSEINEKDLRKKSQELQNALNRQIYYNNEKAITENKESDDQFLENTLLFKGPFPTG 60
Db 1 SEKSEINEKDLRKKSQELQNTA--GNKQIYYNNEKAITENKESHQDFLQHTILFKGPFPTD 58
Qy 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
Db 59 HSWYNDLLVDPSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 118
Qy 121 EKKVPINLWIDGKOTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 119 EKKVPINLWIDGKQNTVPLETVKTKNGVTVQELDLQARRYLQEKYLNYSNVDVDFGKVQ 178
Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSNLHIDLTYTT 233
Db 179 RGLIVFHTSTSPSVNYDLFGAQQYSNTLLRIYRDNKTINSNMHIDIYLYTS 231

RESULT 27
US-08-882-431-2
; Sequence 2, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
```

```

; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431-2

Query Match 79.4%; Score 983; DB 8; Length 257;
Best Local Similarity 79.8%; Pred. No. 1.6e-81;
Matches 186; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKKSQELQNALNRQIYYNNEKAITENKESDDQFLENTLLFKGPFPTG 60
Db 25 SEKSEINEKDLRKKSQGTALGNLQIYYNNEKAITENKESHQDFRQHTILFKGPFPTD 84
Qy 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVRPDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
Qy 121 EKKVPINLWIDGKOTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EKKVPINLWIDGKQNTVPLETVKTKNGVTVQELDLQARRYLQEKYLNYSNVDVDFGKVQ 204
Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSNLHIDLTYTT 233
Db 205 RGLIVFHTSTSPSVNYDLFGAQQYSNTLLRIYRDNKTINSNMHIDIYLYTS 257

RESULT 28
US-08-882-431-4
; Sequence 4, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
```

```
/ CITY: FORT DETRICK
/ STATE: MARYLAND
/ COUNTRY: USA
/ ZIP: 21702-5012
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: Apple Macintosh
/ OPERATING SYSTEM: Macintosh 7.5
/ SOFTWARE: Microsoft Word 6.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/882,431
/ FILING DATE: June 25, 1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Moran, John
/ REGISTRATION NUMBER: 26,313
/ REFERENCE/DOCKET NUMBER:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 619-2065
/ TELEFAX: (301) 619-7714
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 233
/ TYPE: Amino Acid
/ STRANDEDNESS: Unknown
/ TOPOLOGY: Unknown
/ MOLECULE TYPE: Peptide
/ US-08-882-431-4

Query Match 79.0%; Score 978; DB 8; Length 233;
Best Local Similarity 79.3%; Pred. No. 4e-81;
Matches 184; Conservative 17; Mismatches 31; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 61
Db 2 EKSEINEKDLRKSEKQGTALGNLQIYYNEKAITENKESDDQPROHTILFKGFFTDH 61
QY 62 PWYNDLLVDSKDATNKYKGVVQVQAGGTPNKTACMYGGVTLHNNRLTE 121
Db 62 SWYNDLLVDFSDKDIYDKYKGVVQVQAGGTPNKTACMYGGVTLHNNRLTE 121
QY 122 EKQVPIINLWDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVOR 181
Db 122 EKQVPIINLWDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVOR 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGQYPTLLRIYRDNKTINSENHLIDLYLYTT 233
Db 182 GLIVFHTSTEPSVNYDLFGAGQGSNTLLRIYRDNKTINSENHIDIYLYTS 233

RESULT 29
US-10-997-690-11
/ Sequence 11, Application US/10997690
/ Publication No. US20050153376A1
/ GENERAL INFORMATION:
/ APPLICANT: FRASER, JOHN DAVID
/ APPLICANT: PROFT, THOMAS
/ TITLE OF INVENTION: SUPERNATIGENS
/ CURRENT APPLICATION NUMBER: US/10/997,690
/ CURRENT FILING DATE: 2004-11-24
/ PRIOR APPLICATION NUMBER: 09/869,136
/ PRIOR FILING DATE: 2001-07-20
/ PRIOR APPLICATION NUMBER: PCT/NZ99/00228
/ PRIOR FILING DATE: 1999-12-24
/ PRIOR APPLICATION NUMBER: NZ 333589
/ PRIOR FILING DATE: 1998-12-24
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 11

Query Match 67.0%; Score 830; DB 16; Length 268;
Best Local Similarity 64.9%; Pred. No. 1.7e-67;
Matches 150; Conservative 38; Mismatches 43; Indels 0; Gaps 0;

QY 3 KSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQPLENTLLFKGFFTGHP 62
Db 27 KNETIKENLHKSELSITLNNLRHIYFNEKISEKIMTEDEQFLDYTLFKSFFISHS 86
QY 63 WYNDLLVDSKDATNKYKGVVQVQAGGTPNKTACMYGGVTLHNNRLTEE 122
Db 87 QYNDLLVQDSKETVKNKFGKQVDLYGSGYFQCGGKPNKTACMYGGVTLHENNQLYDT 146
QY 123 KKVPINLWDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVOR 182
Db 147 KKIPINLWDSIRTVVPLDIVTKNKKKVTIQELDLQARYLYLHKQYLNINPSTFDGKIQKG 206
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/ LENGTH: 227
/ TYPE: PRT
/ ORGANISM: Streptococcus aureus
/ US-10-997-690-11

Query Match 74.4%; Score 921; DB 18; Length 227;
Best Local Similarity 79.4%; Pred. No. 6.3e-76;
Matches 185; Conservative 17; Mismatches 25; Indels 6; Gaps 6;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 59
QY 61 HPWYNDLLVDSKDATNKYKGVVQVQAGGTPNKTACMYGGVTLHNNRLT 120
Db 60 HSWYNDLLVDFSDKDIYDKYKGVVQVQAGGTPNKTACMY-GVTLHNNRLT 118
QY 121 BEKVPINLWDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 119 EEKVPINLWDG-KONTVPLETNKNKNTVQVQAGGTPNKTACMY-YLQEKYML-NSDVFQKQV 175
QY 181 RGLIVFHSSEGSTVSYDLFDAQGQYPTLLRIYRDNKTINSENHLIDLYLYTT 233
Db 176 RGLIVFHTSTEPSVNYDLFGAGQGSNTLLRIYRDNKTINSENHIDIYLYTS 227

RESULT 30
US-10-428-817A-175
/ Sequence 175, Application US/10428817A
/ Publication No. US20040214783A1
/ GENERAL INFORMATION:
/ APPLICANT: TERMAN, David S
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
/ FILE REFERENCE: 38373-189118
/ CURRENT APPLICATION NUMBER: US/10/428,817A
/ CURRENT FILING DATE: 2003-05-05
/ PRIOR APPLICATION NUMBER: US 60/378,988
/ PRIOR FILING DATE: 2002-05-08
/ PRIOR APPLICATION NUMBER: US 60/389,366
/ PRIOR FILING DATE: 2002-06-15
/ PRIOR APPLICATION NUMBER: US 60/406,697
/ PRIOR FILING DATE: 2002-08-28
/ PRIOR APPLICATION NUMBER: US 60/406,750
/ PRIOR FILING DATE: 2002-08-29
/ PRIOR APPLICATION NUMBER: US 60/415,310
/ PRIOR FILING DATE: 2002-10-01
/ PRIOR APPLICATION NUMBER: US 60/415,400
/ PRIOR FILING DATE: 2002-10-02
/ PRIOR APPLICATION NUMBER: US 60/438,686
/ PRIOR FILING DATE: 2003-01-09
/ NUMBER OF SEQ ID NOS: 224
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 175
/ LENGTH: 268
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
/ US-10-428-817A-175

Query Match 67.0%; Score 830; DB 16; Length 268;
Best Local Similarity 64.9%; Pred. No. 1.7e-67;
Matches 150; Conservative 38; Mismatches 43; Indels 0; Gaps 0;

QY 3 KSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQPLENTLLFKGFFTGHP 62
Db 27 KNETIKENLHKSELSITLNNLRHIYFNEKISEKIMTEDEQFLDYTLFKSFFISHS 86
QY 63 WYNDLLVDSKDATNKYKGVVQVQAGGTPNKTACMYGGVTLHNNRLTEE 122
Db 87 QYNDLLVQDSKETVKNKFGKQVDLYGSGYFQCGGKPNKTACMYGGVTLHENNQLYDT 146
QY 123 KKVPINLWDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVOR 182
Db 147 KKIPINLWDSIRTVVPLDIVTKNKKKVTIQELDLQARYLYLHKQYLNINPSTFDGKIQKG 206
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; SEQ ID NO 34
; LENGTH: 82
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin E
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-34

Query Match 36.9%; Score 457; DB 14; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.6e-34;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 SDDQFLENTLLFKGFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYGYQCAGGTPN 102
Db 1 SDDQFLENTLLFKGFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYGYQCAGGTPN 60

Qy 103 KTACMYGGVTLHDNNRLTEKK 124
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 38
US-10-767-687-19
; Sequence 19, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-767-687-19

Query Match 36.9%; Score 457; DB 17; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.6e-34;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 SDDQFLENTLLFKGFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYGYQCAGGTPN 102

Db 1 SDDQFLENTLLFKGFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYGYQCAGGTPN 60

Qy 103 KTACMYGGVTLHDNNRLTEKK 124
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 39
US-10-002-784A-32
; Sequence 32, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002.784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 32
; LENGTH: 82
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin A
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-32

Query Match 32.2%; Score 399; DB 14; Length 82;
Best Local Similarity 86.6%; Pred. No. 9.2e-29;
Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 43 SDDQFLENTLLFKGFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYGYQCAGGTPN 102
Db 1 SHDQFLQHTLLFKGFTDHSWYNDLLVDFDSKDIDVKYKGKKVDLYGAYGYQCAGGTPN 60

Qy 103 KTACMYGGVTLHDNNRLTEKK 124
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 40
US-10-767-687-17
; Sequence 17, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-767-687-19

Query Match 36.9%; Score 457; DB 17; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.6e-34;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 SDDQFLENTLLFKGFTGHPWYNDLLVDLGSKDATNKYKGKKVDLYGAYGYQCAGGTPN 102

32 NLRNFANYQPEKQGVSSGNFSTSHQLE---YIDGKTYLTSQPH-----NEV 76
81 KGK-----KVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 135
77 EAKRLKDHKVDIFGIGSYGLC-----NTKMYGGITLANQN-LDKPRNIPINLWNGKQ 129
136 TTVPIDKVKTSKKEVTVOELDLQARHYLHGRFGLN-----SDSFGGKVQRCGL 183
130 NTISTDKVSTOKKEVTAQAEIDIKRLRYLQNEYNIYGFNKKYQEGYKSKFNSGFKGK 189
184 IVFHSSEGSTVSVDLFDAGQGVPTDLLRIYRDNKTINSNLHIDL 228
190 ITFHLNNEPSFYDLYFTGTGQAESFLKIYNDKNTIDAENFHLDV 234

Query Match 25.8%; Score 320; DB 16; Length 239;
Best Local Similarity 33.0%; Pred. No. 6.3e-21;
Matches 72; Conservative 40; Mismatches 78; Indels 28; Gaps 6;
25 NLRQIYYNEKAITENK--ESDDQFLENTLLFKGFTGHPWYNLLVDLGSKDATNKYKG 82
28 NLRN--YGSYPEDHQISINPENNLHSLQVFS-----MDNSTVTAEKPNVDVKKFKN 79
83 KVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDK 142
80 HAVDVYGLSYGYCL-----KNKYIYGGVTL-AGDYLEKSRIPINLWNGSHQTISTDK 133
143 VKTSKKEVTVOELDLQARHYLHGRFGLY-----NSDSFGGKVQRCGLIVFHSSE 190
134 VSTNKKLVTAQAEIDIKRLRYLQNEYNIYGFNKTGKNYKSKFSSGFGNAGKILFHLND 193
191 GSTVSVDLFDAGQGVPTDLLRIYRDNKTINSNLHIDL 228
194 GSSFSYDLYFTGTGQAESFLKIYNDKNTVETEKFHLDV 231

RESULT 47
US-10-428-817A-172
; Sequence 172, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 172
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-172

Query Match 25.8%; Score 319.5; DB 16; Length 242;
Best Local Similarity 33.8%; Pred. No. 7.1e-21;
Matches 76; Conservative 35; Mismatches 71; Indels 43; Gaps 8;
25 NLRQIYY-YYNEK--AITENKESDDQFLENTLLFKGFTGHPWYNLLVDLGSKDATNKY 80

Db 32 NLRNFANYQPEKQGVSSGNFSTSHQLE---YIDGKTYLTSQPH-----NEV 76
QY 81 KGK-----KVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 135
Db 77 EAKRLKDHKVDIFGIGSYGLC-----NTKMYGGITLANQN-LDKPRNIPINLWNGKQ 129
QY 136 TTVPIDKVKTSKKEVTVOELDLQARHYLHGRFGLN-----SDSFGGKVQRCGL 183
Db 130 NTISTDKVSTOKKEVTAQAEIDIKRLRYLQNEYNIYGFNKKYQEGYKSKFNSGFKGK 189
QY 184 IVFHSSEGSTVSVDLFDAGQGVPTDLLRIYRDNKTINSNLHIDL 228
Db 190 ITFHLNNEPSFYDLYFTGTGQAESFLKIYNDKNTIDAENFHLDV 234

RESULT 48
US-10-428-817A-176
; Sequence 176, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 176
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-176

Query Match 25.0%; Score 310; DB 16; Length 242;
Best Local Similarity 33.2%; Pred. No. 5.2e-20;
Matches 74; Conservative 39; Mismatches 76; Indels 34; Gaps 9;
QY 23 LSNLRQIY---YYNEKAITENKESDDQFLENTLLFKGFTGHPWYNLLVDLGSKDATN 78
Db 29 IDNLRNFYTKDFINLKVKN-----DTFANQLQF-----SNESY-DLISESKDFNKS 78
QY 79 KYGKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTV 138
Db 79 NFKGKGLDVFGISYNGQC-----NTKYIYGGITA-TNEYLDKPRNIPININWINGHNTI 131
QY 139 PIDKVKTSKKEVTVOELDLQARHYLHGRFGLY-----NSDSFGGK-----VQRCGLIVF 186
Db 132 STNKVSTNKKFVTAQAEIDIKRLRYLQNEYNIYGHNGTKGGEYGHKSKFYGGFNIGKVT 191
QY 187 HSSEGSTVSVDLFDAGQGVPTDLLRIYRDNKTINSNLHIDL 228
Db 192 HLNNDTFSDLYFTGTGDDGLPKSFLKIYEDNKTIVSEKFLDV 234

RESULT 49
US-09-970-759-10
; Sequence 10, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:


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Qy 2 EKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGH 61
Db 1 ESQDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
Qy 62 PWYNDLLVGLSGKDATNKYKGGKVDLYGAYGYQC-----AGTTPNKTACTMYGGV 111
Db 59 GNYDNVRVEFNKDLADKYDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRTKCTMYGGV 118
Qy 112 TLHNNRLTEKKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAAQELDYLTRHYLVKNKKLYE 176
Qy 172 SDSFGGKVQRLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENHLHDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMAPGDKFDQSKYLMYNDNKNMVDSDKVIEVY 233
Qy 230 LYT 232
Db 234 LTT 236
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RESULT 55

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US-09-150-947B-12
; Sequence 12, Application US/09150947B
; Patent No. US20020028211A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
; TITLE OF INVENTION: ANTAGONISTS AND VACCINES
; FILE REFERENCE: A31967-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/150,947B
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-150-947B-12
```

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Query Match 24.2%; Score 299.5; DB 9; Length 239;
Best Local Similarity 33.7%; Pred. No. 4.7e-19;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;
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Qy 2 EKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGH 61
Db 1 ESQDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
Qy 62 PWYNDLLVGLSGKDATNKYKGGKVDLYGAYGYQC-----AGTTPNKTACTMYGGV 111
Db 59 GNYDNVRVEFNKDLADKYDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRTKCTMYGGV 118
Qy 112 TLHNNRLTEKKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAAQELDYLTRHYLVKNKKLYE 176
Qy 172 SDSFGGKVQRLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENHLHDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMAPGDKFDQSKYLMYNDNKNMVDSDKVIEVY 233
Qy 230 LYT 232
Db 234 LTT 236
```

RESULT 56

US-10-172-425B-12

```
; Sequence 12, Application US/10172425B
; Publication No. US20030147908A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
; TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
; FILE REFERENCE: A31967-PCT-USA-A-A 066031.0164
; CURRENT APPLICATION NUMBER: US/10/172,425B
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 09/150,947
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-172-425B-12
```

```
Query Match 24.2%; Score 299.5; DB 14; Length 239;
Best Local Similarity 33.7%; Pred. No. 4.7e-19;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;
```

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Qy 2 EKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGH 61
Db 1 ESQDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
Qy 62 PWYNDLLVGLSGKDATNKYKGGKVDLYGAYGYQC-----AGTTPNKTACTMYGGV 111
Db 59 GNYDNVRVEFNKDLADKYDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRTKCTMYGGV 118
Qy 112 TLHNNRLTEKKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAAQELDYLTRHYLVKNKKLYE 176
Qy 172 SDSFGGKVQRLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENHLHDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMAPGDKFDQSKYLMYNDNKNMVDSDKVIEVY 233
Qy 230 LYT 232
Db 234 LTT 236
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RESULT 57

```
US-10-428-817A-163
; Sequence 163, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
```


Query Match 23.7%; Score 293.5; DB 14; Length 266;
Best Local Similarity 32.8%; Pred. No. 1.9e-18;

Query Match	23.7%	Score 293.5;	DB 17;	Length 266;
Best Local Similarity	32.8%;	Pred. No. 1.9e-18;		
Matches 80: Conservative	45;	Mismatches 100;	Indels 19;	Gaps 7


```
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 16
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURES:
; OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant
US-10-002-784A-16

Query Match      23.4%; Score 289.5; DB 14; Length 251;
Best Local Similarity 33.8%; Pred. No. 4.1e-18;
Matches 80; Conservative 45; Mismatches 93; Indels 19; Gaps 10;

Qy      4 SEENEKDLRKSELRNAL-SNLRIQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
Db      25 SOEFAQQDDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYN---VS 81
Qy      61 HPWNDDLVLGSKDATNKYKGVVDLYGAYGYQC-AGGTPNKTACMYGVTLHDNNRL 119
Db      82 GPNYDKLKTTELKQEMATLFDKKNVDIYGVVEYHLCYLCEAERSACTIYGGVTNHEGNNH 141
Qy      120 TEEKKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKV 179
Db      142 EIPKKIVVKSIDGIQ-SLSFD-IETNKKMWTAQELDYKVRKYLTDNKQLYNGP--SKY 197
Qy      180 QRLGIVFHSSEGSTVSYDLFD---AQQYPTDLLRIYRDNKTINSENHLIDLYLT 232
Db      198 ETGYIKFIPKNKESFWDFPEPEFTOSKY----LMIYKDNETLDSNTSQIEVILTT 250

RESULT 66
US-10-767-687-16
; Sequence 16, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
;           Mark A. Olson
;           Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
;           Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRCM -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
```

```
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-767-687-16

Query Match      23.4%; Score 289.5; DB 17; Length 251;
Best Local Similarity 33.8%; Pred. No. 4.1e-18;
Matches 80; Conservative 45; Mismatches 93; Indels 19; Gaps 10;

Qy      4 SEENEKDLRKSELRNAL-SNLRIQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
Db      25 SOEFAQQDDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYN---VS 81
Qy      61 HPWNDDLVLGSKDATNKYKGVVDLYGAYGYQC-AGGTPNKTACMYGVTLHDNNRL 119
Db      82 GPNYDKLKTTELKQEMATLFDKKNVDIYGVVEYHLCYLCEAERSACTIYGGVTNHEGNNH 141
Qy      120 TEEKKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKV 179
Db      142 EIPKKIVVKSIDGIQ-SLSFD-IETNKKMWTAQELDYKVRKYLTDNKQLYNGP--SKY 197
Qy      180 QRLGIVFHSSEGSTVSYDLFD---AQQYPTDLLRIYRDNKTINSENHLIDLYLT 232
Db      198 ETGYIKFIPKNKESFWDFPEPEFTOSKY----LMIYKDNETLDSNTSQIEVILTT 250

RESULT 67
US-10-002-784A-10
; Sequence 10, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 10
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURES:
; OTHER INFORMATION: mutant staphylococcal enterotoxin B cytoplasmic
US-10-002-784A-10

Query Match      23.3%; Score 288.5; DB 14; Length 239;
Best Local Similarity 33.9%; Pred. No. 4.8e-18;
Matches 80; Conservative 45; Mismatches 88; Indels 23; Gaps 8;

Qy      14 KXSELRNA-----LSNLRIQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLL 68
Db      7 KPDELHKSSKFTGLMNNKVLVDNHNVSAT-NVKSIDQFRYDFDIYSIKDTKLGNDNVR 65
Qy      69 VDLGSKDATNKYKGVVDLYGAYGYQCAGG-----TPNKTACMYGVTLHDNNR 118
Db      66 VEFKNKLADKYDKYVDVFGANNAYQCAFSKKTNDINSHQTDKRTKTCMYGVTHEGNGQ 125
Qy      119 LTEKKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGK 178
Db      126 LDKVRSITVRVFEDGK-NLLSFD-VQTNKKKVTQAELDYLTRHYLVKNKKLYEFNN--SP 181
Qy      179 VQRLGIVFHSSEGSTVSYDLFDAGQGYPD--TLRIYRDNKTINSENHLIDLYLT 232
Db      182 YETGYIKFIENENS-FWYDMMPAGDFDQSKYLMYNDNKNQVDSKOVKIEVILTT 236
```

```

; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/10/923,324
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/555,115
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa is unknown.
US-10-923-324-3

Query Match      23.3%; Score 288.5; DB 17; Length 240;
Best Local Similarity 32.1%; Pred. No. 4.8e-18;
Matches 75; Conservative 49; Mismatches 91; Indels 19; Gaps 9;

QY 11 DLKESLQNALSNLRQIYYNKAITENK-ESDDQFLENTLLPKGFTGHPWYNDLLV 69
DB 10 DLKSSSF-TGTMGNM--YLYDDHVSATKVKSVDFKLAHLIYNISDKKLKNDKVT 66
QY 70 DLGSKDATNKYKGVLDLYGAYGYQC-----AGGTENKTACMYGGVTLHNNRLTEE 122
DB 67 ELLNEDLAKKYDEVVDVYGSNYNCYPSSKDNVGVTKGKTCMYGGITKEGHNFDNG 126
QY 123 --KKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGK 180
DB 127 NLQNLVRVY-ENKRNITISFE-VQTDKKSVAQAELDIKARNFLINKNLNLYEFNS--SPYE 182
QY 181 RGLIVFHSSEGSTVSYDLFDAQQGYPD--TLRIYRDNKTINSENHLIDLXYLT 232
DB 183 TGYIKFIENNGNTFOYDMMFAPGDFQSKYLMYNDNKTVDKSVKIEVHLTT 236

RESULT 70
US-08-882-431-10
; Sequence 10, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MPMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:

; Publication No. US10767687
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MPMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-767-687-10

Query Match      23.3%; Score 288.5; DB 17; Length 239;
Best Local Similarity 33.9%; Pred. No. 4.8e-18;
Matches 80; Conservative 45; Mismatches 88; Indels 23; Gaps 8;

QY 14 KKSELQNA-----LSNLRLQIYYNKAITENKESDDQFLENTLLPKGFTGHPWYNDLL 68
DB 7 KPDELHKSSKFTGLMENMKVLYDDNHVSAI-NVKSIDQFRYFDLYISIKDTKLGNDNR 65
QY 69 VDLGSKDATNKYKGVLDLYGAYGYQCAGG-----TPNKTACMYGGVTLHNNR 118
DB 66 VEPFNKDLADKYKDYVDVFGANAYYQCAFSKKTNDINSHQTDKRTKMYGGVTEHNGNQ 125
QY 119 LTEEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGK 178
DB 126 LDKRSITVRVFDGK-NLLSFD-VQTNKKKVAQAELDYLRHYLVKNKKLYEFNN--SP 181
QY 179 VQRGLIVFHSSEGSTVSYDLFDAQQGYPD--TLRIYRDNKTINSENHLIDLXYLT 232
DB 182 YETGYIKFIENENS-FWYDMMFAPGDFQSKYLMYNDNKNKVDKDKVIEVLYLT 236

RESULT 69
US-10-923-324-3
; Sequence 3, Application US/10923324
```

```

; Publication No. US20050026272A1
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/10/923,324
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/555,115
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa is unknown.
US-10-923-324-3

Query Match      23.3%; Score 288.5; DB 17; Length 240;
Best Local Similarity 32.1%; Pred. No. 4.8e-18;
Matches 75; Conservative 49; Mismatches 91; Indels 19; Gaps 9;

QY 11 DLKESLQNALSNLRQIYYNKAITENK-ESDDQFLENTLLPKGFTGHPWYNDLLV 69
DB 10 DLKSSSF-TGTMGNM--YLYDDHVSATKVKSVDFKLAHLIYNISDKKLKNDKVT 66
QY 70 DLGSKDATNKYKGVLDLYGAYGYQC-----AGGTENKTACMYGGVTLHNNRLTEE 122
DB 67 ELLNEDLAKKYDEVVDVYGSNYNCYPSSKDNVGVTKGKTCMYGGITKEGHNFDNG 126
QY 123 --KKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGK 180
DB 127 NLQNLVRVY-ENKRNITISFE-VQTDKKSVAQAELDIKARNFLINKNLNLYEFNS--SPYE 182
QY 181 RGLIVFHSSEGSTVSYDLFDAQQGYPD--TLRIYRDNKTINSENHLIDLXYLT 232
DB 183 TGYIKFIENNGNTFOYDMMFAPGDFQSKYLMYNDNKTVDKSVKIEVHLTT 236

RESULT 70
US-08-882-431-10
; Sequence 10, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MPMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-10

Query Match 23.2%; Score 287.5; DB 8; Length 239;
Best Local Similarity 33.9%; Pred. No. 5.9e-18; Indels 23; Gaps 8;
Matches 80; Conservative 45; Mismatches 88;

Qy 14 KKSEIQRNA-----LSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLL 68
Db 7 KPDELHKSSKSTGKWMKNKVLDDNHVSAL-NVKSIDQFRYFDLIYSIKDTKLGNYDNVR 65

Qy 69 VLGSKDATNKYKGGKVDLYGAYGYQCAGG-----TPNKTACMYGGVTLHNNR 118
Db 66 VEFKNKDLADKYKDYVDVFGANAYYQCAFSSKTKTNDINSHQTDKRRKTCMYGGVTEHNGQ 125

Qy 119 LTBKKVPLNLDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFLGYNDSFGK 178
Db 126 LDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDLTRHYLVKDKKLYEFNN--SP 181

Qy 179 VQGLIVFHSSEGSTVSYDLFDAQQYDP--TLRLIYRDNKTINSNLHIDLILYT 232
Db 182 YETGVIKIEIENS-FWDDMPAPGDKFDQSKYLMYNDNKWDSKDVKIEVILTT 236

RESULT 71
US-10-923-324-6
; Sequence 6, Application US/10923324
; Publication No. US20050026272A1
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/10/923,324
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/555,115
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa is unknown.
US-10-923-324-6

Query Match 23.2%; Score 287.5; DB 17; Length 240;
Best Local Similarity 32.1%; Pred. No. 5.9e-18; Indels 19; Gaps 9;
Matches 75; Conservative 48; Mismatches 92;

Qy 11 DLKKSEIQRNA--LYDDHYVSATKVKSVDFLAHDLIYNISDKLKNYDKVKT 66
Db 70 DLGSKDATNKYKGGKVDLYGAYGYQC-----AGTTPNKTACMYGGVTLHNNRLEE 122
Db 67 ELLNEDLAKKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGGKTCMYGGITKHEGNHFDNG 126
Qy 123 --KKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFLGYNDSFGK 180
Db 127 NLQNVLRVY-ENKNTISFE-VQTDKSVTAQELDIKARNFLINKKNLYEFNS--SPYE 182
Qy 181 RGLIVFHSSEGSTVSYDLFDAQQYDP--TLRLIYRDNKTINSNLHIDLILYT 232
Db 183 TGYIKFTIENNGNTFOYDMMPPAPGDKFDQSKYLMYNDNKTVDSKRVKIEVILTT 236

RESULT 72
US-10-923-324-5
; Sequence 5, Application US/10923324
; Publication No. US20050026272A1
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/10/923,324
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/555,115
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa is unknown.
US-10-923-324-5

Query Match 23.1%; Score 285.5; DB 17; Length 240;
Best Local Similarity 31.3%; Pred. No. 9e-18; Indels 19; Gaps 9;
Matches 76; Conservative 49; Mismatches 99;

Qy 2 EKSEINEKDLRKSEIQRNA--LYDDHYVSATKVKSVDFLAHDLIYNISDKK 57
Db 1 ESQPDPTFDELHKSEF-TGTMGNMK--LYDDHYVSATKVKSVDFLAHDLIYNISDKK 57
Qy 61 HPWYNDLLVGLSKDATNKYKGGKVDLYGAYGYQC-----AGTTPNKTACMYGGVTL 113
Db 58 LKNYDKVKTELLNEDLAKKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGGKTCMYGGITK 117
Qy 114 HDNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFLGYN 171
Db 118 HEGNHFDNGNLQNLIRVY-ENKNTISFE-VQTDKSVTAQELDIKARNFLINKKNLYE 175
Qy 172 SDSFGKVGQRLIVFHSSEGSTVSYDLFDAQQYDP--TLRLIYRDNKTINSNLHIDL 229
Db 176 FNS--SPYETGYIKFTIENNGNTFOYDMMPPAPGDKFDQSKYLMYNDNKTVDSKRVKIEVH 233
Qy 230 LYT 232
Db 234 LTT 236

RESULT 73
US-10-428-817A-186
; Sequence 186, Application US/10428817A
; Publication No. US20040214783A1
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-10

Query Match 23.2%; Score 287.5; DB 8; Length 239;
Best Local Similarity 33.9%; Pred. No. 5.9e-18; Indels 23; Gaps 8;
Matches 80; Conservative 45; Mismatches 88;

Qy 14 KKSEIQRNA-----LSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLL 68
Db 7 KPDELHKSSKSTGKWMKNKVLDDNHVSAL-NVKSIDQFRYFDLIYSIKDTKLGNYDNVR 65

Qy 69 VLGSKDATNKYKGGKVDLYGAYGYQCAGG-----TPNKTACMYGGVTLHNNR 118
Db 66 VEFKNKDLADKYKDYVDVFGANAYYQCAFSSKTKTNDINSHQTDKRRKTCMYGGVTEHNGQ 125

Qy 119 LTBKKVPLNLDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFLGYNDSFGK 178
Db 126 LDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDLTRHYLVKDKKLYEFNN--SP 181

Qy 179 VQGLIVFHSSEGSTVSYDLFDAQQYDP--TLRLIYRDNKTINSNLHIDLILYT 232
Db 182 YETGVIKIEIENS-FWDDMPAPGDKFDQSKYLMYNDNKWDSKDVKIEVILTT 236

RESULT 71
US-10-923-324-6
; Sequence 6, Application US/10923324
; Publication No. US20050026272A1
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/10/923,324
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/555,115
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa is unknown.
US-10-923-324-6

Query Match 23.2%; Score 287.5; DB 17; Length 240;
Best Local Similarity 32.1%; Pred. No. 5.9e-18; Indels 19; Gaps 9;
Matches 75; Conservative 48; Mismatches 92;

Qy 11 DLKKSEIQRNA--LYDDHYVSATKVKSVDFLAHDLIYNISDKLKNYDKVKT 66
Db 70 DLGSKDATNKYKGGKVDLYGAYGYQC-----AGTTPNKTACMYGGVTLHNNRLEE 122
Db 67 ELLNEDLAKKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGGKTCMYGGITKHEGNHFDNG 126
Qy 123 --KKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFLGYNDSFGK 180
Db 127 NLQNVLRVY-ENKNTISFE-VQTDKSVTAQELDIKARNFLINKKNLYEFNS--SPYE 182
Qy 181 RGLIVFHSSEGSTVSYDLFDAQQYDP--TLRLIYRDNKTINSNLHIDLILYT 232
Db 183 TGYIKFTIENNGNTFOYDMMPPAPGDKFDQSKYLMYNDNKTVDSKRVKIEVILTT 236

RESULT 72
US-10-923-324-5
; Sequence 5, Application US/10923324
; Publication No. US20050026272A1
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/10/923,324
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/555,115
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa is unknown.
US-10-923-324-5

Query Match 23.1%; Score 285.5; DB 17; Length 240;
Best Local Similarity 31.3%; Pred. No. 9e-18; Indels 19; Gaps 9;
Matches 76; Conservative 49; Mismatches 99;

Qy 2 EKSEINEKDLRKSEIQRNA--LYDDHYVSATKVKSVDFLAHDLIYNISDKK 57
Db 1 ESQPDPTFDELHKSEF-TGTMGNMK--LYDDHYVSATKVKSVDFLAHDLIYNISDKK 57
Qy 61 HPWYNDLLVGLSKDATNKYKGGKVDLYGAYGYQC-----AGTTPNKTACMYGGVTL 113
Db 58 LKNYDKVKTELLNEDLAKKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGGKTCMYGGITK 117
Qy 114 HDNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFLGYN 171
Db 118 HEGNHFDNGNLQNLIRVY-ENKNTISFE-VQTDKSVTAQELDIKARNFLINKKNLYE 175
Qy 172 SDSFGKVGQRLIVFHSSEGSTVSYDLFDAQQYDP--TLRLIYRDNKTINSNLHIDL 229
Db 176 FNS--SPYETGYIKFTIENNGNTFOYDMMPPAPGDKFDQSKYLMYNDNKTVDSKRVKIEVH 233
Qy 230 LYT 232
Db 234 LTT 236

RESULT 73
US-10-428-817A-186
; Sequence 186, Application US/10428817A
; Publication No. US20040214783A1
```


STREET: US Army MRC - 504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 265
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-6

Query Match 22.6%; Score 280; DB 8; Length 265;
Best Local Similarity 31.6%; Pred. No. 3.3e-17;
Matches 77; Conservative 45; Mismatches 102; Indels 20; Gaps 7;
QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 27 ASQPPKPEDELHKSKEF--TGLMEDMKVLYDDNHVSAINVKSIDQLFYDLIYSIKDK 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGG 110
DB 85 LGDYDNVRVEFKMKDLADKYKVDVFGVYNYCYQYFYSKKTNDINSHQDKRKTQMYG 144
QY 111 VTLHDNNRLTEEEKVPINLWIDGKQTVPIDKVKTSKEVTVQELDLQARHYLHGKFLY 170
DB 145 VTEHNGNQLDKYSITVRVFDGK--NLLGPD--VQYNNKKVTAQELDYLTRHYLVKNKKLY 202
QY 171 NSDSFGKVQORGLIVFHSSEGSTVSVDLPDAQOQ--YPTDLLRIYRDNKTINSNLHIDL 228
DB 203 EFN--SPYETGYIKF--TENQNFWDMPAPGDKFAQSKYLMYNDNKNKVDKVKLEV 258
QY 229 YLYT 232
DB 259 YLTT 262

RESULT 79
US-10-923-324-7
Sequence 7, Application US/10923324
Publication No. US20050026272A1
GENERAL INFORMATION:
APPLICANT: Bohach, Gregory I.
TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
FILE REFERENCE: 12136.1USWO
CURRENT APPLICATION NUMBER: US/10/923,324
CURRENT FILING DATE: 2004-08-20
PRIORITY APPLICATION NUMBER: US/09/555,115
PRIORITY FILING DATE: 2000-08-01
PRIORITY APPLICATION NUMBER: PCT/US98/25107
PRIORITY FILING DATE: 1998-12-01
PRIORITY APPLICATION NUMBER: US 60/067,357

PRIOR FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patent in version 3.1
SEQ ID NO 7
LENGTH: 240
TYPE: PRT
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (240)..(240)
OTHER INFORMATION: Xaa is unknown.
US-10-923-324-7

Query Match 22.3%; Score 276.5; DB 17; Length 240;
Best Local Similarity 30.5%; Pred. No. 6e-17;
Matches 74; Conservative 52; Mismatches 98; Indels 19; Gaps 9;
QY 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENK-ESDDQFLENTLLFKGFFTG 60
DB 1 ESQPDTPDELHKSKEF--TGLMENMKVL--YDRYVSATKVKSVDFLAHLDIYINISDKK 57
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGGVTL 113
DB 58 LKDYDKVTELLNEDLAKYKDEVVDVYGSNYVNCYFSDKNVGVKTCMYGGITK 117
QY 114 HDNNRLTEE--KKVPINLWIDGKQTVPIDKVKTSKEVTVQELDLQARHYLHGKFLY 171
DB 118 HEGNHPDNGNLQNLIRVY--ENKRNITISPE--VQTDKKS VTAQELDIKARNFLINKKNLYE 175
QY 172 SDSFGKVQORGLIVFHSSEGSTVSVDLPDAQOQYD--TLLRIYRDNKTINSNLHIDL 229
DB 176 FNS--SPYETGYIKF--TENQNFWDMPAPGDKFQSKYLMYNDNKNKVDKVKLEV 233
QY 230 LYT 232
DB 234 LTT 236

RESULT 80
US-10-923-324-8
Sequence 8, Application US/10923324
Publication No. US20050026272A1
GENERAL INFORMATION:
APPLICANT: Bohach, Gregory I.
TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
FILE REFERENCE: 12136.1USWO
CURRENT APPLICATION NUMBER: US/10/923,324
CURRENT FILING DATE: 2004-08-20
PRIORITY APPLICATION NUMBER: US/09/555,115
PRIORITY FILING DATE: 2000-08-01
PRIORITY APPLICATION NUMBER: PCT/US98/25107
PRIORITY FILING DATE: 1998-12-01
PRIORITY APPLICATION NUMBER: US 60/067,357
PRIORITY FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patent in version 3.1
SEQ ID NO 8
LENGTH: 240
TYPE: PRT
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (240)..(240)
OTHER INFORMATION: Xaa is unknown.
US-10-923-324-8

Query Match 22.3%; Score 276.5; DB 17; Length 240;
Best Local Similarity 30.5%; Pred. No. 6e-17;
Matches 74; Conservative 52; Mismatches 98; Indels 19; Gaps 9;
QY 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENK-ESDDQFLENTLLFKGFFTG 60
DB 1 ESQPDTPDELHKSKEF--TGLMENMKVL--YDRYVSATKVKSVDFLAHLDIYINISDKK 57

61	Qy	HPWYNDLLVDLGSKDATNKGKGVKVDLYGAYGYQC-----AGGTNPNTKTCMYGGVTL	113
58	Db	LKNYDKVKTELLNEDLAKYKDEVDVVGSGSYNYNCCFFSKDNVGVKVTGGKTCMYGGITK	117
114	Qy	HDNNRLTEE--KKVPINLWDGKQTTPVIDKVKTSKKEVTVQELDLOARHVLHGKFGFLYN	171
118	Db	HEGHHFONGNLQNVLIRYV-ENKNTISFE-VQTDKKSVTAEGLDKARNFELINKNLYE	175
172	Qy	SDSPGGKVGQRGLIVFHSSEGSTVSVDLFDAGQYPD--TLRLRYRDNKNTINSENLHIDL	229
176	Db	FNS--SPYETGYIKFIEENNNGNTFYQDMMPAFGDKFDQSKYLMYNDNKTVDTSKRVKIEVH	233
230	Qy	LYT	232
234	Db	LTT	236

RESULT 81
US-08-882-431-8
; Sequence 8, Application US/08882431
; Publication NO. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MPMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

```

      |::| :| :|| :||| :||| :||| :||| :| :| :|||
85  LGDYDNVRVEPKNLDADKYKDKYVDVFGANAYQCAFSSKKTNDINSHQTDXRKTCMYGG 144

      |::| :| :|| :||| :||| :||| :||| :||| :||| :|||
111 VTLHDNRLTEKKVPINLWIDGQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKEGLY 170

      |::| :| :|| :||| :||| :||| :||| :||| :||| :|||
145 VTEHNGQLDKYRSITVRVFPEDGK-NLLSFD-VQYNKKVTAQELDYLTRHYLVKNKCLY 202

      |::| :| :|| :||| :||| :||| :||| :||| :||| :|||
171 NSDSFGKQVBQGLIVFHSSEGSTVSYDLFDAQQYPD--TLRLRYRDNKNTINSENHLIDL 228

      |::| :| :|| :||| :||| :||| :||| :||| :||| :|||
203 EFNN--SPYETGYIKF-IENQNFWMMPAGDFDOSKYLMMYNDNKNQVDSKQVKLEV 258

      |::| :| :|| :||| :||| :||| :||| :||| :||| :|||
229 YLYT 232

      |::| :| :|| :||| :||| :||| :||| :||| :||| :|||
259 YLTT 262

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RESULT 82
US-10-428-817A-171
; Sequence 171, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428.817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 171
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
; US-10-428-817A-171

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RESULT 83
US-09-870-759-12
; Sequence 12, Application US/09870759
; Patent No. US20020177551A1

Db 27 AESQDPPTDELHASKF-TGLMENMKVLYDDHYVSATKVK-SVDKFRADHLIYNISDKK 84
Qy 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYYGYQC-----AGTGNKTAACMYGGVTL 113
Db 85 LKNYDKVKTLLNEGLAKKYKDEVDVYGSYVNCYFSSKDNVGVKVTGGKTCMYGGITK 144
Qy 114 HDNNRLTEB--KKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYN 171
Db 145 HEGNHFDNGNLQNLVLRVY-ENKRNITISPE-VQTDKKSVTQAQELDIKARNFLINKKNLYE 202
Qy 172 SDSFGGKVGRLIVFHSSEGSTVSYDLFDAQGYQPD--TLRIYRDNKTINSENHLIDLY 229
Db 203 FNS--SFYETGYIKFTIENNGNTFWYDMMPAPGDKFQSKYLMYNDNKTVDKSKVIEVH 260
Qy 230 LYT 232
Db 261 LTT 263

RESULT 89
US-10-002-784A-14
; Sequence 14, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
/33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 14
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: staphylococcal enterotoxin C-1 mutant
US-10-002-784A-14

Query Match 20.9%; Score 258.5; DB 14; Length 266;
Best Local Similarity 30.0%; Pred. No. 3e-15;
Matches 73; Conservative 51; Mismatches 102; Indels 17; Gaps 8;
Qy 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 27 AESQDPPTDELHASKF-TGLMENMKVLYDDHYVSATKVK-SVDKFRADHLIYNISDKK 84
Qy 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYYGYQC-----AGTGNKTAACMYGGVTL 113
Db 85 LKNYDKVKTLLNEGLAKKYKDEVDVYGSYVNCYFSSKDNVGVKVTGGKTCMYGGITK 144
Qy 114 HDNNRLTEB--KKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYN 171
Db 145 HEGNHFDNGNLQNLVLRVY-ENKRNITISPE-VQTDKKSVTQAQELDIKARNFLINKKNLYE 202
Qy 172 SDSFGGKVGRLIVFHSSEGSTVSYDLFDAQGYQPD--TLRIYRDNKTINSENHLIDLY 229
Db 203 FNS--SFYETGYIKFTIENNGNTFWYDMMPAPGDKFQSKYLMYNDNKTVDKSKVIEVH 260
Qy 230 LYT 232
Db 261 LTT 263

RESULT 90
US-10-767-687-14
; Sequence 14, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:

APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA: US/10/767,687
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 266
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-767-687-14

Query Match 20.9%; Score 258.5; DB 17; Length 266;
Best Local Similarity 30.0%; Pred. No. 3e-15;
Matches 73; Conservative 51; Mismatches 102; Indels 17; Gaps 8;
Qy 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 27 AESQDPPTDELHASKF-TGLMENMKVLYDDHYVSATKVK-SVDKFRADHLIYNISDKK 84
Qy 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYYGYQC-----AGTGNKTAACMYGGVTL 113
Db 85 LKNYDKVKTLLNEGLAKKYKDEVDVYGSYVNCYFSSKDNVGVKVTGGKTCMYGGITK 144
Qy 114 HDNNRLTEB--KKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYN 171
Db 145 HEGNHFDNGNLQNLVLRVY-ENKRNITISPE-VQTDKKSVTQAQELDIKARNFLINKKNLYE 202
Qy 172 SDSFGGKVGRLIVFHSSEGSTVSYDLFDAQGYQPD--TLRIYRDNKTINSENHLIDLY 229
Db 203 FNS--SFYETGYIKFTIENNGNTFWYDMMPAPGDKFQSKYLMYNDNKTVDKSKVIEVH 260
Qy 230 LYT 232
Db 261 LTT 263
RESULT 91
US-10-002-784A-26
; Sequence 26, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
/33

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; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 26
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin-A
US-10-002-784A-26

Query Match      20.7%; Score 256.5; DB 14; Length 220;
Best Local Similarity 33.8%; Pred. No. 3.6e-15;
Matches 76; Conservative 43; Mismatches 85; Indels 21; Gaps 12;

Qy 16 SELQRNAL-SNLRLQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFTGHPWYNLDLVDLG 72
Db 8 SQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYN---VSGPNVDKLTTELK 64

Qy 73 SKDATNKYKGKVDLYGAYGYOC-AGGTPNKACMYGVTTLHDNNRLTEEEKVPINLWI 131
Db 65 NQEMATLFDKDNIDYGVVEYHLYCYLENAERSACI-GGVTNREGNHLEIPKKIVVKVSI 123

Qy 132 DGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFLYNSDFGKVGQRLIVFHSSEG 191
Db 124 DGIO-SLSFD-IETNKKMVTQAELDYKVRKYLTDNKKQLYTNGP--SKYETGYIKFIPKNK 179

Qy 192 STVSVDLFD-----AQOGYPDTLLRIYRDKNKTINSENHLIDLXYLT 232
Db 180 ESFWDFPEPEFTQSKI-----LMIYKDNETLDS-NTQIEVYLTT 219

RESULT 92
US-10-002-784A-27
; Sequence 27, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 27
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant SpeA-mutant SpeB fusion
US-10-002-784A-27

Query Match      20.7%; Score 256.5; DB 14; Length 468;
Best Local Similarity 33.8%; Pred. No. 9.7e-15;
Matches 76; Conservative 43; Mismatches 85; Indels 21; Gaps 12;

Qy 16 SELQRNAL-SNLRLQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFTGHPWYNLDLVDLG 72
Db 8 SQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYN---VSGPNVDKLTTELK 64

Qy 73 SKDATNKYKGKVDLYGAYGYOC-AGGTPNKACMYGVTTLHDNNRLTEEEKVPINLWI 131
Db 65 NQEMATLFDKDNIDYGVVEYHLYCYLENAERSACI-GGVTNREGNHLEIPKKIVVKVSI 123

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; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-428-817A-16

Query Match      19.8%; Score 245; DB 16; Length 250;
Best Local Similarity 30.7%; Pred. No. 4.8e-14;
Matches 70; Conservative 42; Mismatches 94; Indels 22; Gaps 9;

Qy 14 KKSLEQNALSNLRQIYYNEKA--IT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVD 70
Db 35 KPSQLQSNLVKTKPIYFFMRVTLVTHENVKSVQDQLSHDLIYN---VSGPNYDKLTKTE 91
Qy 71 LGSKDATNKYKGGKVDLYGAYGYQC-AGGTPNKACMYGGVTLHDNNRLTEKKVPINL 129
Db 92 LKNQEMATLFDKKNVDIYGVVEYHLYLCENASACLYGGVTNHEGHNHLEIPKKIVVKV 151
Qy 130 WIDSKQT-TVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVGRLIVPHS 188
Db 152 SIDGIQSLSFIEQIKNG---NCSRSISYTVRKYLTDNKQLYTNGP--SKYETGYIKFIP 205
Qy 189 SEGSTVSVDLPD---AQGYPDTLRLRYRDNKTINSENHLIDLYLVT 232
Db 206 KNKESFWDFPPEPFTQSKY----LMIYKDNETLDSNTSQIEVLYLT 249

RESULT 98
US-10-937-758A-20
; Sequence 20, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-937-758A-20

Query Match      19.8%; Score 245; DB 17; Length 250;
Best Local Similarity 30.7%; Pred. No. 4.8e-14;
Matches 70; Conservative 42; Mismatches 94; Indels 22; Gaps 9;

Qy 14 KKSLEQNALSNLRQIYYNEKA--IT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVD 70
Db 35 KPSQLQSNLVKTKPIYFFMRVTLVTHENVKSVQDQLSHDLIYN---VSGPNYDKLTKTE 91
Qy 71 LGSKDATNKYKGGKVDLYGAYGYQC-AGGTPNKACMYGGVTLHDNNRLTEKKVPINL 129
Db 92 LKNQEMATLFDKKNVDIYGVVEYHLYLCENASACLYGGVTNHEGHNHLEIPKKIVVKV 151
Qy 130 WIDSKQT-TVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVGRLIVPHS 188
Db 152 SIDGIQSLSFIEQIKNG---NCSRSISYTVRKYLTDNKQLYTNGP--SKYETGYIKFIP 205
Qy 189 SEGSTVSVDLPD---AQGYPDTLRLRYRDNKTINSENHLIDLYLVT 232
Db 206 KNKESFWDFPPEPFTQSKY----LMIYKDNETLDSNTSQIEVLYLT 249

RESULT 99
US-10-428-817A-169
; Sequence 169, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 169
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-428-817A-169

Query Match      19.3%; Score 239; DB 16; Length 209;
Best Local Similarity 27.0%; Pred. No. 1.3e-13;
Matches 65; Conservative 48; Mismatches 62; Indels 66; Gaps 10;

Qy 17 ELQRNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVD----- 70
Db 2 EVDNNSL--LRNIY-----STIVVE-----YSDTVIDPFKTSNN 32
Qy 71 -----LGSKDATNKYKGGKVDLYCAY-----YGVQACAGGTPNKACMYG 109
Db 33 LVTKKLDVRDARDPFFINSEMDYAADFKAGDKIAVSPDPWNYLSKG---KVTAYTYG 89
Qy 110 GVTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFG 169
Db 90 GITPYQKTSI--PKNIPVNLWLNKQIPVPVQINQISTNKTVTTAQEIDLKVRKFLIAQ 147
Qy 170 YNSDSFGGKVGRLIVPHSSEGS--TVSYVDLPDAQGYPDTLRLRYRDNKTINSENHL-HID 227
Db 148 YSS---GSSYKSGKLVFHTDNDNSDKYSLDLFYTGYRDKESIFKVYKDNKSFNIDKIGH 204
Qy 228 L 228
Db 205 I 205

RESULT 100
US-10-428-817A-184
; Sequence 184, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
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; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 184
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-184

Query Match          17.8%; Score 220.5; DB 16; Length 240;
Best Local Similarity 29.7%; Pred. No. 7.9e-12;
Matches              63; Conservative 42; Mismatches 92; Indels 15; Gaps 7;

QY      1  SEKSEINEKDLKKSELQNALSNLRQIYYVNEKAITENKESDDOFLENTLFFKGFFTG 60
Db      27  AESQDPTPELHKASKF-TGLMENMKVLDDHVVSATVK-SVDKFLAHLDIYNSDKK 84

QY      61  HPWYNLLVDLGSKDATNKYGGKKVDLYGAYGVQC-----AGTPNKATCMYGGVTL 113
Db      85  LKNYDKVKYTELLNEGLAKTYKDEVDVDYGSNNYVNCYFSSKDNVKGVTGSKTCMYGGITK 144

QY      114  HDNNRLTEE--KKVPINLWIDGQTTPVIDOKVTSKKEVTWQBLDLOARHYLHGKFGLYN 171
Db      145  HEGNHDPNGNLQNLIVFY-ENKENTISFE-VQTDKKSVAQELDIKARNFLINKKNLYE 202

QY      172  SDSFGGKVGKGLIVFHSSEGSTVSYDLFDAQG 203
Db      203  FNS--GPYETGYIKFIENNGNTWIDMWPAPG 232

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Search completed: July 26, 2005, 11:21:16
Job time : 164 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2005, 11:01:24 ; Search time 22 Seconds
(without alignments)
790.601 Million cell updates/sec

Title: US-09-900-766-7

Perfect score: 1238

Sequence: 1 SEKSEINEKDLKKSELR.....RDNKTINSENLHLYLTYT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/prodata/1/aaa/5B-COMB.pep:*
3: /cgn2_6/prodata/1/aaa/6A-COMB.pep:*
4: /cgn2_6/prodata/1/aaa/6B-COMB.pep:*
5: /cgn2_6/prodata/1/aaa/PCUS-COMB.pep:*
6: /cgn2_6/prodata/1/aaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1238	100.0	233	4	US-08-695-692B-8
2	1238	100.0	257	3	US-08-486-099-112
3	1238	100.0	257	3	US-08-360-107A-122
4	1238	100.0	257	3	US-08-484-223B-112
5	1238	100.0	257	3	US-08-919-597-112
6	1238	100.0	257	3	US-08-475-668A-112
7	1238	100.0	257	3	US-08-485-551A-112
8	1238	100.0	257	3	US-08-471-913A-112
9	1238	100.0	257	3	US-08-485-264A-112
10	1238	100.0	257	3	US-08-474-349A-112
11	1238	100.0	257	4	US-08-470-896-112
12	1238	100.0	257	4	US-08-485-546A-112
13	1238	100.0	257	4	US-08-487-266A-112
14	1202	97.1	254	4	US-09-350-841A-1598
15	1171	94.6	226	3	US-08-896-933-24
16	1171	94.6	226	3	US-09-314-235-24
17	1171	94.6	226	3	US-09-708-008B-24
18	1023	82.6	233	4	US-08-695-692B-7
19	1023	82.6	257	3	US-08-486-099-113
20	1023	82.6	257	3	US-08-360-107A-123
21	1023	82.6	257	3	US-08-484-223B-113
22	1023	82.6	257	3	US-08-919-597-113
23	1023	82.6	257	3	US-08-475-668A-113
24	1023	82.6	257	3	US-08-485-551A-113
25	1023	82.6	257	3	US-08-471-913A-113
26	1023	82.6	257	3	US-08-485-264A-113
27	1023	82.6	257	3	US-08-474-349A-113

28	1023	82.6	257	4	US-08-470-896-113	Sequence 113, Appl
29	1023	82.6	257	4	US-08-485-546A-113	Sequence 113, Appl
30	1023	82.6	257	4	US-08-487-266A-113	Sequence 113, Appl
31	1019	82.3	233	1	US-08-446-918A-4	Sequence 4, Appl1
32	1019	82.3	233	2	US-08-580-806-4	Sequence 4, Appl1
33	1003.5	81.1	232	3	US-08-896-933-23	Sequence 23, Appl
34	1003.5	81.1	232	3	US-09-314-235-23	Sequence 23, Appl
35	1003.5	81.1	232	3	US-09-708-008B-23	Sequence 23, Appl
36	1000	80.8	257	3	US-09-144-776B-2	Sequence 2, Appl1
37	1000	80.8	257	3	US-08-882-431B-2	Sequence 2, Appl1
38	996	80.5	233	3	US-09-144-776B-4	Sequence 4, Appl1
39	996	80.5	233	3	US-08-882-431B-4	Sequence 4, Appl1
40	926.5	74.8	252	4	US-09-350-841A-1599	Sequence 1599, Ap
41	657	53.1	228	3	US-08-896-933-25	Sequence 25, Appl
42	657	53.1	228	3	US-09-314-235-25	Sequence 25, Appl
43	657	53.1	228	4	US-09-708-008B-25	Sequence 25, Appl
44	457	36.9	82	3	US-09-144-776B-19	Sequence 19, Appl
45	457	36.9	82	3	US-08-882-431B-19	Sequence 19, Appl
46	399	32.2	82	3	US-09-144-776B-17	Sequence 17, Appl
47	399	32.2	82	4	US-08-882-431B-17	Sequence 17, Appl
48	300	24.2	255	1	US-08-446-918A-2	Sequence 2, Appl1
49	300	24.2	255	2	US-08-580-806-2	Sequence 2, Appl1
50	296.5	23.9	221	3	US-08-896-933-29	Sequence 29, Appl
51	296.5	23.9	221	3	US-09-314-235-29	Sequence 29, Appl
52	296.5	23.9	221	4	US-09-708-008B-29	Sequence 29, Appl
53	294.5	23.8	251	4	US-08-973-391C-13	Sequence 13, Appl
54	293.5	23.7	266	3	US-09-144-776B-6	Sequence 6, Appl1
55	293.5	23.7	266	4	US-08-882-431B-6	Sequence 6, Appl1
56	292.5	23.6	239	3	US-08-896-933-26	Sequence 26, Appl
57	292.5	23.6	239	3	US-09-314-235-26	Sequence 26, Appl
58	292.5	23.6	239	4	US-09-708-008B-26	Sequence 26, Appl
59	292.5	23.6	266	3	US-09-414-276-8	Sequence 8, Appl1
60	291.5	23.5	221	4	US-08-973-391C-14	Sequence 14, Appl
61	289.5	23.4	251	3	US-09-144-776B-16	Sequence 16, Appl
62	289.5	23.4	251	4	US-08-882-431B-16	Sequence 16, Appl
63	288.5	23.3	239	3	US-09-144-776B-10	Sequence 10, Appl
64	288.5	23.3	239	4	US-08-882-431B-10	Sequence 10, Appl
65	282.5	22.8	266	3	US-09-144-776B-8	Sequence 8, Appl1
66	282.5	22.8	266	4	US-08-882-431B-8	Sequence 8, Appl1
67	281.5	22.7	238	3	US-08-896-933-28	Sequence 28, Appl
68	281.5	22.7	238	3	US-09-314-235-28	Sequence 28, Appl
69	281.5	22.7	238	4	US-09-708-008B-28	Sequence 28, Appl
70	267.5	21.6	239	3	US-08-896-933-27	Sequence 27, Appl
71	267.5	21.6	239	3	US-09-314-235-27	Sequence 27, Appl
72	267.5	21.6	239	4	US-09-708-008B-27	Sequence 27, Appl
73	260.5	21.0	239	3	US-08-896-933-21	Sequence 21, Appl
74	260.5	21.0	239	3	US-09-314-235-21	Sequence 21, Appl
75	260.5	21.0	239	4	US-09-708-008B-21	Sequence 21, Appl
76	258.5	20.9	266	3	US-09-144-776B-14	Sequence 14, Appl
77	258.5	20.9	266	4	US-08-882-431B-14	Sequence 14, Appl
78	245	19.8	220	3	US-08-896-933-20	Sequence 20, Appl
79	245	19.8	220	3	US-09-314-235-20	Sequence 20, Appl
80	245	19.8	220	4	US-09-708-008B-20	Sequence 20, Appl
81	215	17.4	82	3	US-09-144-776B-18	Sequence 18, Appl
82	215	17.4	82	4	US-08-882-431B-18	Sequence 18, Appl
83	191	15.4	45	1	US-08-220-378-1	Sequence 1, Appl1
84	191	15.4	45	2	US-08-696-012-1	Sequence 1, Appl1
85	183.5	14.8	235	4	US-09-336-036-2	Sequence 2, Appl1
86	183.5	14.8	235	4	US-09-308-829-2	Sequence 2, Appl1
87	181.5	14.7	208	3	US-08-896-933-30	Sequence 30, Appl
88	181.5	14.7	208	3	US-09-314-235-30	Sequence 30, Appl
89	181.5	14.7	208	4	US-09-708-008B-30	Sequence 30, Appl
90	137.5	11.1	89	3	US-09-144-776B-20	Sequence 20, Appl
91	137.5	11.1	89	4	US-08-882-431B-20	Sequence 20, Appl
92	129	10.4	28	1	US-08-220-378-2	Sequence 2, Appl1
93	129	10.4	28	2	US-08-696-012-2	Sequence 2, Appl1
94	127	10.3	24	3	US-08-838-413A-22	Sequence 22, Appl
95	126	10.2	23	1	US-08-220-378-5	Sequence 5, Appl1
96	126	10.2	23	2	US-08-696-012-5	Sequence 5, Appl1
97	124	10.0	29	1	US-08-220-378-6	Sequence 6, Appl1
98	124	10.0	29	2	US-08-696-012-6	Sequence 6, Appl1
99	121	9.8	79	3	US-09-144-776B-24	Sequence 24, Appl
100	121	9.8	79	4	US-08-882-431B-24	Sequence 24, Appl

101	120	9.7	22	1	US-08-220-378-4	Sequence 4, Appl	174	89	7.2	631	3	US-08-897-438-115	Sequence 115, Appl
102	120	9.7	22	2	US-08-696-012-4	Sequence 4, Appl	175	89	7.2	631	3	US-08-637-654-115	Sequence 115, Appl
103	112.5	9.1	89	3	US-09-144-776B-22	Sequence 22, Appl	176	89	7.2	631	3	US-08-649-518-115	Sequence 115, Appl
104	112.5	9.1	89	3	US-09-144-776B-23	Sequence 23, Appl	177	87.5	7.1	629	4	US-09-248-796A-19860	Sequence 19860, A
105	112.5	9.1	89	4	US-08-882-431B-22	Sequence 22, Appl	178	87	7.0	286	3	US-09-134-001C-4103	Sequence 4103, Ap
106	112.5	9.1	89	4	US-08-882-431B-23	Sequence 23, Appl	179	86.5	7.0	258	4	US-09-107-532A-4002	Sequence 4002, Ap
107	111.5	9.0	443	4	US-09-710-279-1860	Sequence 1860, Ap	180	86.5	7.0	834	1	US-08-471-033-21	Sequence 21, Appl
108	110.5	8.9	444	3	US-09-134-001C-4346	Sequence 4346, Ap	181	86.5	7.0	834	2	US-08-471-044-21	Sequence 21, Appl
109	110	8.9	23	1	US-08-220-378-10	Sequence 10, Appl	182	86.5	7.0	834	2	US-08-463-483A-21	Sequence 21, Appl
110	110	8.9	23	2	US-08-696-012-10	Sequence 10, Appl	183	86.5	7.0	834	2	US-08-471-046A-21	Sequence 21, Appl
111	109	8.8	27	3	US-08-896-933-34	Sequence 34, Appl	184	86.5	7.0	834	2	US-08-470-566B-21	Sequence 21, Appl
112	109	8.8	27	3	US-09-314-235-34	Sequence 34, Appl	185	86.5	7.0	834	2	US-08-469-334-21	Sequence 21, Appl
113	109	8.8	27	4	US-09-708-008B-34	Sequence 34, Appl	186	86.5	7.0	834	2	US-09-300-529-21	Sequence 21, Appl
114	109	8.8	193	3	US-08-896-933-31	Sequence 31, Appl	187	85	6.9	17	3	US-08-896-933-10	Sequence 10, Appl
115	109	8.8	193	3	US-09-314-235-31	Sequence 31, Appl	188	85	6.9	17	3	US-09-314-235-10	Sequence 10, Appl
116	109	8.8	193	4	US-09-708-008B-31	Sequence 31, Appl	189	85	6.9	17	4	US-09-708-008B-10	Sequence 10, Appl
117	109	8.8	229	4	US-09-350-841A-1597	Sequence 1597, Ap	190	84.5	6.8	228	4	US-09-710-279-1166	Sequence 1166, Ap
118	107.5	8.7	234	3	US-08-486-099-111	Sequence 111, App	191	84.5	6.8	406	4	US-09-134-000C-3752	Sequence 3752, Ap
119	107.5	8.7	234	3	US-08-360-107A-121	Sequence 121, App	192	84.5	6.8	1588	5	PCT-US93-07261-11	Sequence 11, Appl
120	107.5	8.7	234	3	US-08-484-223B-111	Sequence 111, App	193	84.5	6.8	1663	5	PCT-US93-07261-16	Sequence 16, Appl
121	107.5	8.7	234	3	US-08-919-537-111	Sequence 111, App	194	84	6.8	365	3	US-09-134-001C-4412	Sequence 4412, Ap
122	107.5	8.7	234	3	US-08-475-668A-111	Sequence 111, App	195	84	6.8	558	4	US-09-902-540-14971	Sequence 14971, A
123	107.5	8.7	234	3	US-08-485-551A-111	Sequence 111, App	196	84	6.8	675	3	US-09-134-001C-4547	Sequence 4547, Ap
124	107.5	8.7	234	3	US-08-471-913A-111	Sequence 111, App	197	84	6.8	1014	4	US-09-762-724-2	Sequence 2, Appl
125	107.5	8.7	234	3	US-08-485-264A-111	Sequence 111, App	198	83.5	6.7	251	4	US-09-543-681A-6514	Sequence 6514, Ap
126	107.5	8.7	234	3	US-08-474-349A-111	Sequence 111, App	199	83.5	6.7	752	4	US-09-710-279-1138	Sequence 1138, Ap
127	107.5	8.7	234	4	US-08-470-896-111	Sequence 111, App	200	83.5	6.7	767	3	US-09-134-001C-4023	Sequence 4023, Ap
128	107.5	8.7	234	4	US-08-485-546A-111	Sequence 111, App							
129	107.5	8.7	234	4	US-08-487-266A-111	Sequence 111, App							
130	106.5	8.6	29	1	US-08-220-378-9	Sequence 9, Appl							
131	106.5	8.6	29	1	US-08-696-012-9	Sequence 9, Appl							
132	106	8.6	28	1	US-08-220-378-7	Sequence 7, Appl							
133	106	8.6	28	2	US-08-696-012-7	Sequence 7, Appl							
134	105.5	8.5	89	3	US-09-144-776B-21	Sequence 21, Appl							
135	105.5	8.5	89	4	US-08-882-431B-21	Sequence 21, Appl							
136	105.5	8.5	194	1	US-08-446-918A-6	Sequence 6, Appl							
137	105.5	8.5	194	2	US-08-580-806-6	Sequence 6, Appl							
138	105	8.5	25	1	US-08-220-378-3	Sequence 3, Appl							
139	105	8.5	25	2	US-08-696-012-3	Sequence 3, Appl							
140	104.5	8.4	234	3	US-09-144-776B-12	Sequence 12, Appl							
141	104.5	8.4	234	4	US-08-882-431B-12	Sequence 12, Appl							
142	100.5	8.1	234	1	US-08-153-456A-2	Sequence 2, Appl							
143	100.5	8.1	234	1	US-08-440-221-2	Sequence 2, Appl							
144	100	8.1	28	1	US-08-220-378-8	Sequence 8, Appl							
145	100	8.1	28	2	US-08-696-012-8	Sequence 8, Appl							
146	94.5	7.6	402	3	US-09-134-001C-4674	Sequence 4674, Ap							
147	93.5	7.6	631	1	US-08-487-890A-111	Sequence 111, App							
148	93.5	7.6	631	2	US-08-478-435-111	Sequence 111, App							
149	93.5	7.6	631	2	US-08-337-483-111	Sequence 111, App							
150	93.5	7.6	631	3	US-08-478-373-111	Sequence 111, App							
151	93.5	7.6	631	3	US-08-474-671-111	Sequence 111, App							
152	93.5	7.6	631	3	US-08-483-577A-111	Sequence 111, App							
153	93.5	7.6	631	3	US-08-897-438-111	Sequence 111, App							
154	93.5	7.6	631	3	US-08-637-654-111	Sequence 111, App							
155	93.5	7.6	631	3	US-08-649-518-111	Sequence 111, App							
156	93	7.5	16	4	US-08-695-692B-20	Sequence 20, Appl							
157	93	7.5	28	3	US-08-896-933-22	Sequence 22, Appl							
158	93	7.5	28	3	US-09-314-235-22	Sequence 22, Appl							
159	93	7.5	28	4	US-09-708-008B-22	Sequence 22, Appl							
160	92.5	7.5	337	4	US-09-248-796A-16723	Sequence 16723, A							
161	92.5	7.5	1183	4	US-09-532-310B-5	Sequence 5, Appl							
162	89.5	7.2	36	3	US-08-838-413A-7	Sequence 7, Appl							
163	89.5	7.2	38	3	US-08-838-413A-8	Sequence 8, Appl							
164	89	7.2	24	3	US-08-838-413A-18	Sequence 18, Appl							
165	89	7.2	171	4	US-09-710-279-1074	Sequence 1074, Ap							
166	89	7.2	179	3	US-09-134-001C-3300	Sequence 3300, Ap							
167	89	7.2	317	4	US-09-248-796A-19212	Sequence 19212, A							
168	89	7.2	631	1	US-08-487-890A-115	Sequence 115, App							
169	89	7.2	631	2	US-08-478-435-115	Sequence 115, App							
170	89	7.2	631	2	US-08-337-483-115	Sequence 115, App							
171	89	7.2	631	2	US-08-478-373-115	Sequence 115, App							
172	89	7.2	631	3	US-08-474-671-115	Sequence 115, App							
173	89	7.2	631	3	US-08-483-577A-115	Sequence 115, App							

ALIGNMENTS

RESULT 1
 US-08-695-692B-8
 ; Sequence 8, Application US/08695692B
 ; Patent No. 6514498
 ; GENERAL INFORMATION:
 ; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlstén,
 ; APPLICANT: Johan Hansson, Terje Kalland, Lars
 ; APPLICANT: Abrahamson and Goran Forsberg
 ; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
 ; STREET: 1177 West Loop South, 10th Floor
 ; CITY: Houston
 ; STATE: TX
 ; COUNTRY: USA
 ; ZIP: 77027-9095
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/695,692B
 ; FILING DATE: August 12, 1996
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 9601245-5
 ; FILING DATE: March 29, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Krieger, Paul E.
 ; REGISTRATION NUMBER: 25,886
 ; REFERENCE/DOCKET NUMBER: 41986/1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713-850-0909
 ; TELEFAX: 713-850-0165
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 233 amino acids
 ; TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-695-692B-8

Query Match 100.0%; Score 1238; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 9.3e-119; Indels 0; Gaps 0;
Matches 233; Conservative 0; Mismatches 0;
QY 1 SEKSEINEKDLRKKESELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKKESELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIDLYLTT 233
DB 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIDLYLTT 233

RESULT 2
US-08-486-099-112
Sequence 112, Application US/08486099
Patent No. 6013263

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
TITLE OF INVENTION: B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-486-099-112

Query Match 100.0%; Score 1238; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKESELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKESELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFFTG 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIDLYLTT 233
DB 205 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIDLYLTT 257

RESULT 3
US-08-360-107A-122
Sequence 122, Application US/08360107A
Patent No. 6017536

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-360-107A-122

Query Match 100.0%; Score 1238; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;

Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGPF TG 60
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGPF TG 84
Qy 61 HPWYNDLLVLDGSDATNKYKGVVDLYGAYYGQCAGGTPNKTCACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVLDGSDATNKYKGVVDLYGAYYGQCAGGTPNKTCACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
Qy 181 RGLIVFHSSEGSTVSYDLFDAQQGVPDTLLRIYRDNKTINSENHLIDLYLTT 233
Db 205 RGLIVFHSSEGSTVSYDLFDAQQGVPDTLLRIYRDNKTINSENHLIDLYLTT 257

RESULT 4
US-08-484-223B-112
; Sequence 112, Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 245
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-484-223B-112

Query Match 100.0%; Score 1238; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGPF TG 60

Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGPF TG 84
Qy 61 HPWYNDLLVLDGSDATNKYKGVVDLYGAYYGQCAGGTPNKTCACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVLDGSDATNKYKGVVDLYGAYYGQCAGGTPNKTCACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
Qy 181 RGLIVFHSSEGSTVSYDLFDAQQGVPDTLLRIYRDNKTINSENHLIDLYLTT 233
Db 205 RGLIVFHSSEGSTVSYDLFDAQQGVPDTLLRIYRDNKTINSENHLIDLYLTT 257

RESULT 5
US-08-919-597-112
; Sequence 112, Application US/08919597
; Patent No. 6054265
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,597
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,896
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-919-597-112

Query Match 100.0%; Score 1238; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGPF TG 60

Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRLRIYRDNKTINSENHLIDLYLYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRLRIYRDNKTINSENHLIDLYLYTT 257

RESULT 6

US-08-475-668A-112
; Sequence 112, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Pettaway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,668A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-475-668A-112

Query Match 100.0%; Score 1238; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCACMYGGVTLHDNNRLT 144

QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRLRIYRDNKTINSENHLIDLYLYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRLRIYRDNKTINSENHLIDLYLYTT 257

RESULT 7

US-08-485-551A-112
; Sequence 112, Application US/08485551A
; Patent No. 6068973
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Pettaway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,551A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-551A-112

Query Match 100.0%; Score 1238; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

Qy	181	RG	LI	PH	SS	RG	ST	VS	YL	FD	AQ	QY	PD	TL	RI	YR	DN	KT	IN	SE	NH	DI	LV	LT	233
Dp	205	RG	LI	PH	SS	RG	ST	VS	YL	FD	AQ	QY	PD	TL	RI	YR	DN	KT	IN	SE	NH	DI	LV	LT	257

```

RESULT 8
US-08-471-913A-112
; Sequence 112, Application US/08471913A
; Patent No. 6093794
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,913A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-471-913A-112

Query Match 100.0%; Score 1238; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELQARNLSNRQIYYNEKAITENKSDQFLENTLLFKGFTG 60
Db 25 SEKSEINEKDLRKSELQARNLSNRQIYYNEKAITENKSDQFLENTLLFKGFTG 84
Qy 61 HPWYNLLVDLGSKDATNKYKGKVDLYGAYGYQCAGGTPNKTCMTGGVTLHNNRLT 120
Db 85 HPWYNLLVDLGSKDATNKYKGKVDLYGAYGYQCAGGTPNKTCMTGGVTLHNNRLT 144
Qy 121 EEKKVPINLWIDCKQTTPVDIKVTSKEVTYQELDLQARHYLHGKFLYNSDSFGKVQ 180
Db 145 EEKKVPINLWIDCKQTTPVDIKVTSKEVTYQELDLQARHYLHGKFLYNSDSFGKVQ 204
Qy 181 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRNNKTINSNLHIDLYLTT 233

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Db      205  RGLIVFHSSSGSTVSVDLFDPAQCGYDPTLLRIYRDNKTINSENHLDLYLYTT 23
      205  RGLIVFHSSSGSTVSVDLFDPAQCGYDPTLLRIYRDNKTINSENHLDLYLYTT 23

RESULT 9
US-08-485-264A-112
; Sequence 112, Application US/08485264A
; Patent No. 622983
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,264A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8964
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-485-264A-112

Query Match      100.0%; Score 1238; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      1  SEKSEETNEKDLRKKSELQNALSNLRQIYYNYNEKAITENKESDDQFLENTLLFKG
      25  SEKSEETNEKDLRKKSELQNALSNLRQIYYNYNEKAITENKESDDQFLENTLLFKG
Db      61  HPWYNLLVDLGSKDATNKYKGKVDLYGAYYGCAGGTPNKTCAMYGCVTLHDNN
      85  HPWYNLLVDLGSKDATNKYKGKVDLYGAYYGCAGGTPNKTCAMYGCVTLHDNN
Qy      121  BEKKVPINLWIDGQTTVPIDKVKTSKKEVTVOQLDQARHYLHGKFGLYNSDSFG
      145  BEKKVPINLWIDGQTTVPIDKVKTSKKEVTVOQLDQARHYLHGKFGLYNSDSFG
Db      181  RGLIVFHSSSGSTVSVDLFDPAQCGYDPTLLRIYRDNKTINSENHLDLYLYTT 233
      205  RGLIVFHSSSGSTVSVDLFDPAQCGYDPTLLRIYRDNKTINSENHLDLYLYTT 235

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RESULT 10
 US-08-474-349A-112
 ; Sequence 112, Application US/08474349A
 ; Patent No. 6333395
 ; GENERAL INFORMATION:
 ; APPLICANT: Bolognesi, Dani P.
 ; APPLICANT: Matthews, Thomas J.
 ; APPLICANT: Wild, Carl T.
 ; APPLICANT: Barney, Shawn O.
 ; APPLICANT: Lambert, Dennis M.
 ; APPLICANT: Pettaway, Stephen R.
 ; APPLICANT: Langlois, Alphonse J.
 ; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
 ; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
 ; TITLE OF INVENTION: VIRUS TRANSMISSION
 ; NUMBER OF SEQUENCES: 517
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/474,349A
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7872-024
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 112:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 257 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-474-349A-112

Query Match 100.0%; Score 1238; DB 3; Length 257;
 Best Local Similarity 100.0%; Pred. No. 1.1e-118;
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELRNALSRLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKSELRNALSRLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
 QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
 DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
 QY 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 180
 DB 145 EEKVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 204
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQYQPDTLRLRIYRDNKTINSENLHIDLVLTYT 233
 DB 205 RGLIVFHSSEGSTVSVDLFDAGQYQPDTLRLRIYRDNKTINSENLHIDLVLTYT 257

RESULT 11
 US-08-470-896-112
 ; Sequence 112, Application US/08470896

Patent No. 6479055
 ; GENERAL INFORMATION:
 ; APPLICANT: Bolognesi, Dani P.
 ; APPLICANT: Matthews, Thomas J.
 ; APPLICANT: Wild, Carl T.
 ; APPLICANT: Barney, Shawn O.
 ; APPLICANT: Lambert, Dennis M.
 ; APPLICANT: Pettaway, Stephen R.
 ; APPLICANT: Langlois, Alphonse J.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
 ; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
 ; NUMBER OF SEQUENCES: 273
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/470,896
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7872-020
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 112:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 257 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-470-896-112

Query Match 100.0%; Score 1238; DB 4; Length 257;
 Best Local Similarity 100.0%; Pred. No. 1.1e-118; Indels 0; Gaps 0;
 Matches 233; Conservative 0; Mismatches 0;

QY 1 SEKSEINEKDLRKSELRNALSRLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKSELRNALSRLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
 QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
 DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
 QY 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 180
 DB 145 EEKVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 204
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQYQPDTLRLRIYRDNKTINSENLHIDLVLTYT 233
 DB 205 RGLIVFHSSEGSTVSVDLFDAGQYQPDTLRLRIYRDNKTINSENLHIDLVLTYT 257

RESULT 12
 US-08-485-546A-112
 ; Sequence 112, Application US/08485546A
 ; Patent No. 6518013
 ; GENERAL INFORMATION:
 ; APPLICANT: Bolognesi, Dani P.

```
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,546A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-546A-112

Query Match 100.0%; Score 1238; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.le-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELQNALNLRQIYYNEKAITENKESDDQFLENTLLFKGFFT 60
Db 25 SEKSEINEKDLRKSELQNALNLRQIYYNEKAITENKESDDQFLENTLLFKGFFT 84

Qy 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 144

Qy 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLOARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLOARHYLHGKFGLYNSDSFGGKVQ 204

Qy 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNKTINSENHLDILYLYTT 233
Db 205 RGLIVFHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNKTINSENHLDILYLYTT 257

RESULT 13
US-08-487-266A-112
; Sequence 112, Application US/08487266A
; Patent No. 6824783
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.

; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,266A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-487-266A-112

Query Match 100.0%; Score 1238; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.le-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELQNALNLRQIYYNEKAITENKESDDQFLENTLLFKGFFT 60
Db 25 SEKSEINEKDLRKSELQNALNLRQIYYNEKAITENKESDDQFLENTLLFKGFFT 84

Qy 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 144

Qy 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLOARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLOARHYLHGKFGLYNSDSFGGKVQ 204

Qy 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNKTINSENHLDILYLYTT 233
Db 205 RGLIVFHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNKTINSENHLDILYLYTT 257

RESULT 14
US-09-350-841A-1598
; Sequence 1598, Application US/09350841A
; Patent No. 6750008
; GENERAL INFORMATION:
; APPLICANT: Jeffes, Peter;
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; FILE REFERENCE: 7872-066-999
; CURRENT APPLICATION NUMBER: US/09/350.841A
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 1946
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 1598
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-350-841A-1598

Query Match      97.1%; Score 1202; DB 4; Length 254;
Best Local Similarity 98.3%; Pred. No. 5.2e-115;
Matches 230; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 SESEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
DB 22 SESEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 81
QY 61 HPWYNDLLVGLGSKDATNKYKGGVDLYGAYGYQCAGTGNKATCMYGGVTLHNNRLT 120
DB 82 HPWYNDLLVGLGSKDATNKYKGGVDLYGAYGYQCAGTGNKATCMYGGVTLHNNRLT 141
QY 121 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 142 BEKVPINLWID-KQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 200
QY 181 RGLIVFHSSEG-STVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIDLYTT 233
DB 201 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIDLYTT 254

RESULT 15
US-08-896-933-24
; Sequence 24, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-24

Query Match      94.6%; Score 1171; DB 3; Length 226;
Best Local Similarity 95.7%; Pred. No. 6.6e-112;
Matches 220; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 4 SESEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHPW 63
DB 1 SESEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHPW 60
QY 64 YNDLLVGLGSKDATNKYKGGVDLYGAYGYQCAGTGNKATCMYGGVTLHNNRLTEK 123
DB 61 YNDLLVGLGSKDATNKYKGGVDLYGAYGYQCAGTGNKATCMYGGVTLHNNRLTEK 119
QY 124 KVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 183
DB 120 ---VBKWIWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 176
QY 184 IVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIDLYTT 233
DB 177 IVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIDLYTT 226

RESULT 17
US-09-708-008B-24
; Sequence 24, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; EARLIER FILING DATE: 2000-11-08
; EARLIER APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-708-008B-24

Query Match      94.6%; Score 1171; DB 4; Length 226;
Best Local Similarity 95.7%; Pred. No. 6.6e-112;

QY 4 SESEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHPW 63
DB 1 SESEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHPW 60
QY 64 YNDLLVGLGSKDATNKYKGGVDLYGAYGYQCAGTGNKATCMYGGVTLHNNRLTEK 123
DB 61 YNDLLVGLGSKDATNKYKGGVDLYGAYGYQCAGTGNKATCMYGGVTLHNNRLTEK 119
QY 124 KVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 183
DB 120 ---VBKWIWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 176
QY 184 IVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIDLYTT 233
DB 177 IVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIDLYTT 226

RESULT 16
US-09-314-235-24
; Sequence 24, Application US/09314235
; Patent No. 6338845
```

Matches 220; Conservative 4; Mismatches 2; Indels 4; Gaps 1;
Qy 4 SEENEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFTGHPW 63
Db 1 SEENEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFTGHPW 60
Qy 64 YNDLVLGSKDATNKYKGGKVDLYGAYGYQCAGGTENKTAACMYGGVTLHDNNRLTEK 123
Db 61 YNDLVLGSKDATNKYKGGKVDLYGAYGYQCAGGTENKTAACMYGGVTLHDNNRLTEE- 119
Qy 124 KVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQRL 183
Db 120 ---VBKWIIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQRL 176
Qy 184 IVFHSSEGSTVSVDLFDAGQGVPTLLRIYRDNKTINSENHIDILYLYTT 233
Db 177 IVFHSSEGSTVSVDLFDAGQGVPTLLRIYRDNKTINSENHIDILYLYTT 226

RESULT 18
US-08-695-692B-7
; Sequence 7, Application US/08695692B
; Patent No. 6514498
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlaten,
; APPLICANT: Johan Hansson, Terje Kalland, Lars
; APPLICANT: Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; TITLE OF INVENTION: AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695.692B
; FILING DATE: August 12, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-695-692B-7

Query Match 82.6%; Score 1023; DB 4; Length 233;
Best Local Similarity 82.0%; Pred. No. 1e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFTG 60
Db 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFTD 60
Qy 61 HPWYNDLVLGSKDATNKYKGGKVDLYGAYGYQCAGGTENKTAACMYGGVTLHDNNRLT 120

Db 61 HSWYNDLVLGSKDATNKYKGGKVDLYGAYGYQCAGGTENKTAACMYGGVTLHDNNRLT 120
Qy 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGVPTLLRIYRDNKTINSENHIDILYLYTT 233
Db 181 RGLIVFHSSEGSTVSVDLFDAGQGVPTLLRIYRDNKTINSENHIDILYLYTS 233

RESULT 19
US-08-486-099-113
; Sequence 113, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; TITLE OF INVENTION: B VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486.099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-486-099-113

Query Match 82.6%; Score 1023; DB 3; Length 257;
Best Local Similarity 82.0%; Pred. No. 1.2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFTG 60
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFTD 84
Qy 61 HPWYNDLVLGSKDATNKYKGGKVDLYGAYGYQCAGGTENKTAACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLVLGSKDATNKYKGGKVDLYGAYGYQCAGGTENKTAACMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 145 EEKVPINLWLDGKQNTVPLETVKTKNKNVTQELDLQARRYLQEKYNLYNSDVFQKQV 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIDLYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAGQYSNTLLRIYRDNKTINSENHIDLYLTS 257

RESULT 20
US-08-360-107A-123
; Sequence 123, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,107A
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-360-107A-123

Query Match 82.6%; Score 1023; DB 3; Length 257;
Best Local Similarity 82.0%; Pred. No. 1.2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDKRKSELOARNLSNLRQIYYNEKAITENKESDDOFLNTLLPKGFFTG 60
Db 25 SEKSEINEKDKRKSELOARNLSNLRQIYYNEKAITENKESDDOFLNTLLPKGFFTG 84
QY 61 HPWYNLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNLLVDFDSKIDVYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 145 EEKVPINLWLDGKQNTVPLETVKTKNKNVTQELDLQARRYLQEKYNLYNSDVFQKQV 204

QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIDLYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAGQYSNTLLRIYRDNKTINSENHIDLYLTS 257

RESULT 21
US-08-484-223B-113
; Sequence 113, Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 245
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-484-223B-113

Query Match 82.6%; Score 1023; DB 3; Length 257;
Best Local Similarity 82.0%; Pred. No. 1.2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDKRKSELOARNLSNLRQIYYNEKAITENKESDDOFLNTLLPKGFFTG 60
Db 25 SEKSEINEKDKRKSELOARNLSNLRQIYYNEKAITENKESDDOFLNTLLPKGFFTG 84
QY 61 HPWYNLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNLLVDFDSKIDVYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 145 EEKVPINLWLDGKQNTVPLETVKTKNKNVTQELDLQARRYLQEKYNLYNSDVFQKQV 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIDLYLTT 233

Db 205 RGLIVFHTSTBPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHMHIDIYLYTS 257

```
RESULT 22
US-08-919-597-113
; Sequence 113, Application US/08919597
; Patent No. 6054265
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,597
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US 08/470,896
; APPLICATION NUMBER: 06-JUN-1995
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-919-597-113

Query Match 82.6%; Score 1023; DB 3; Length 257;
Best Local Similarity 82.0%; Pred. No. 1.2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKXSELQNALNLRQIYYNKAITENKESDDQFLNTLLFKGPFPTG 60
Db 25 SEKSEINEKDLRKXSELQNALNLRQIYYNKAITENKESDDQFLNTLLFKGPFPTD 84

Qy 61 HPWYNDLLVDLGSKDATNKYKGVVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVKYKGVVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 144

Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGGKVQ 180
Db 145 EEKVPINLWLDGKQNTVPLETVKTKNKNVTVPQELDLQARHYLQEKYLNLYNSDVFDPGKVQ 204

Qy 181 RGLIVFHTSSEGSTVSVDLFDAGQGYPTDTLRIYRDNKTINSENHMHIDIYLYTT 233
Db 205 RGLIVFHTSTBPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHMHIDIYLYTS 257
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Db 205 RGLIVFHTSTBPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHMHIDIYLYTS 257

```
RESULT 23
US-08-475-668A-113
; Sequence 113, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,668A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-475-668A-113

Query Match 82.6%; Score 1023; DB 3; Length 257;
Best Local Similarity 82.0%; Pred. No. 1.2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKXSELQNALNLRQIYYNKAITENKESDDQFLNTLLFKGPFPTG 60
Db 25 SEKSEINEKDLRKXSELQNALNLRQIYYNKAITENKESDDQFLNTLLFKGPFPTD 84

Qy 61 HPWYNDLLVDLGSKDATNKYKGVVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVKYKGVVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 144

Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGGKVQ 180
Db 145 EEKVPINLWLDGKQNTVPLETVKTKNKNVTVPQELDLQARHYLQEKYLNLYNSDVFDPGKVQ 204

Qy 181 RGLIVFHTSSEGSTVSVDLFDAGQGYPTDTLRIYRDNKTINSENHMHIDIYLYTT 233
Db 205 RGLIVFHTSTBPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHMHIDIYLYTS 257
```

RESULT 24
US-08-485-551A-113
; Sequence 113, Application US/08485551A
; Patent No. 6068973

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pettaway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-551A-113

Query Match 82.6%; Score 1023; DB 3; Length 257;
Best Local Similarity 82.0%; Pred. No. 1.2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDDLVDLGSKDNTNKGKVDLYGAYGYQCAGTGNKTCACMYGGVTLHDNNRLT 120
DB 85 HSWYNDDLVDLGSKDNTNKGKVDLYGAYGYQCAGTGNKTCACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTPIDKVKTSKKEVTVQELDLQARHYLHGKFGYNSDSFGKVKQ 180
DB 145 BEKKVPINLWIDGKQTPIDKVKTSKKEVTVQELDLQARHYLHGKFGYNSDSFGKVKQ 204
QY 181 RGLIVPHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHLDLYLT 233
DB 205 RGLIVPHSTEPSVNDLFDAGQYPTLLRIYRDNKTINSENHLDLYLT 257

RESULT 25
US-08-471-913A-113
Sequence 113, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pettaway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-471-913A-113

Query Match 82.6%; Score 1023; DB 3; Length 257;
Best Local Similarity 82.0%; Pred. No. 1.2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDDLVDLGSKDNTNKGKVDLYGAYGYQCAGTGNKTCACMYGGVTLHDNNRLT 120
DB 85 HSWYNDDLVDLGSKDNTNKGKVDLYGAYGYQCAGTGNKTCACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTPIDKVKTSKKEVTVQELDLQARHYLHGKFGYNSDSFGKVKQ 180
DB 145 BEKKVPINLWIDGKQTPIDKVKTSKKEVTVQELDLQARHYLHGKFGYNSDSFGKVKQ 204
QY 181 RGLIVPHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHLDLYLT 233
DB 205 RGLIVPHSTEPSVNDLFDAGQYPTLLRIYRDNKTINSENHLDLYLT 257

RESULT 26
US-08-485-264A-113
Sequence 113, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
MOLECULE TYPE: protein
US-08-485-264A-113

Query Match 82.6%; Score 1023; DB 3; Length 257;
Best Local Similarity 82.0%; Pred. No. 1.2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYNKAITENKESDDQFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNKAITENKESDDQFLNTLLFKGFFTD 84
Qy 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDI VDKYKGGKVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPLETVTKNKNVTVQELDLQARRYLQEKYNLYNSDVPDGKVQ 204
Qy 181 RGLIVFHSSEGSTSYDLFDAGQGYPTDLLRIYRDNKTINSNLHIDLTYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAGQGYNTLLRIYRDNKTINSNLHIDLTYLTS 257

RESULT 27
US-08-474-349A-113
Sequence 113, Application US/08474349A
Patent No. 6333395
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barnett, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
MOLECULE TYPE: protein
US-08-474-349A-113

Query Match 82.6%; Score 1023; DB 3; Length 257;
Best Local Similarity 82.0%; Pred. No. 1.2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYNKAITENKESDDQFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNKAITENKESDDQFLNTLLFKGFFTD 84
Qy 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDI VDKYKGGKVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPLETVTKNKNVTVQELDLQARRYLQEKYNLYNSDVPDGKVQ 204
Qy 181 RGLIVFHSSEGSTSYDLFDAGQGYPTDLLRIYRDNKTINSNLHIDLTYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAGQGYNTLLRIYRDNKTINSNLHIDLTYLTS 257

RESULT 28
US-08-470-896-113
Sequence 113, Application US/08470896
Patent No. 6479055
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barnett, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273

CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,896
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-896-113

Query Match 82.6%; Score 1023; DB 4; Length 257;
Best Local Similarity 82.0%; Pred. No. 1.2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 144

QY 121 EKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 EKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204

QY 181 RGLVPHSSEGSTVSVDLFDAGQYPTDILLRIYRDNKNTINSENHLDLYLT 233
DB 205 RGLVPHSTSTEPSVNYDLFAGQYNTLLRIYRDNKNTINSENHLDLYLT 257

RESULT 29
US-08-485-546A-113
Sequence 113, Application US/08485546A
Patent No. 6518013
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-546A-113

Query Match 82.6%; Score 1023; DB 4; Length 257;
Best Local Similarity 82.0%; Pred. No. 1.2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 144

QY 121 EKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 EKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204

QY 181 RGLVPHSSEGSTVSVDLFDAGQYPTDILLRIYRDNKNTINSENHLDLYLT 233
DB 205 RGLVPHSTSTEPSVNYDLFAGQYNTLLRIYRDNKNTINSENHLDLYLT 257

RESULT 30
US-08-487-266A-113
Sequence 113, Application US/08487266A
Patent No. 6824783
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,266A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-487-266A-113

Query Match 82.6%; Score 1023; DB 4; Length 257;
Best Local Similarity 82.0%; Pred. No. 1.2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESHDFLQHTILFKGFFTD 84

Qy 61 HPWNLLVDLGSKDATNKYKGVVQELDQARHYLHGKFLGYNDSFGGKVV 120
Db 85 HSWYNDLLVDFDSKIDVDKYKGVVQELDQARHYLHGKFLGYNDSFGGKVV 144

Qy 121 EEKVPINLWDGKOTTPIDKVTSKKEVTVQELDQARHYLHGKFLGYNDSFGGKVV 180
Db 145 EEKVPINLWDGKQNTVPLETVTKNKNVTVQELDQARHYLHGKFLGYNDSFGGKVV 204

Qy 181 RGLIVFHSSEGSTSVYDLFDAQGYPTDLLRIYRDNKTINSNLHIDLTYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFQAQGYSNLTLRIYRDNKTINSNMHIDIYLYTS 257

RESULT 31
US-08-446-918A-4
; Sequence 4, Application US/08446918A
; Patent No. 5705151
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,918A
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 552
; ATTORNEY/AGENT INFORMATION:

; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-29
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-446-918A-4

Query Match 82.3%; Score 1019; DB 1; Length 233;
Best Local Similarity 81.9%; Pred. No. 2.6e-96;
Matches 190; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

Qy 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFFTG 61
Db 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESHDFLQHTILFKGFFTDH 61

Qy 62 PWYNDLLVDLGSKDATNKYKGVVQELDQARHYLHGKFLGYNDSFGGKVV 121
Db 62 SWYNDLLVDFDSKIDVDKYKGVVQELDQARHYLHGKFLGYNDSFGGKVV 121

Qy 122 EEKVPINLWDGKOTTPIDKVTSKKEVTVQELDQARHYLHGKFLGYNDSFGGKVV 181
Db 122 EEKVPINLWDGKQNTVPLETVTKNKNVTVQELDQARHYLHGKFLGYNDSFGGKVV 181

Qy 182 GLIVFHSSEGSTSVYDLFDAQGYPTDLLRIYRDNKTINSNLHIDLTYTT 233
Db 182 GLIVFHTSTEPSVNYDLFQAQGYSNLTLRIYRDNKTINSNMHIDIYLYTS 233

RESULT 32
US-08-580-806-4
; Sequence 4, Application US/08580806
; Patent No. 5935568
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; APPLICANT: Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear


```
; MOLECULE TYPE: protein
US-08-580-806-4

Query Match      82.3%; Score 1019; DB 2; Length 233;
Best Local Similarity 81.9%; Pred. No. 2.6e-96;
Matches 190; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTTG 61
DB 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTTG 61

QY 62 HWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTTPNKTCMYGGVTLHDNNRLTE 121
DB 62 HWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTTPNKTCMYGGVTLHDNNRLTE 121

QY 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQVOR 181
DB 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQVOR 181

QY 182 GLIVFHSSEGSTVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLHDLYLTT 233
DB 182 GLIVFHSSEGSTVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLHDLYLTT 233

RESULT 33
US-08-896-933-23
; Sequence 23, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT FILING DATE: 1997-07-18
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-23

Query Match      81.1%; Score 1003.5; DB 3; Length 232;
Best Local Similarity 81.5%; Pred. No. 1e-94;
Matches 190; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTTG 60
DB 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTTG 60

QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTTPNKTCMYGGVTLHDNNRLT 120
DB 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTTPNKTCMYGGVTLHDNNRLT 120

QY 121 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 121 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180

QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLHDLYLTT 233
DB 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLHDLYLTT 233

RESULT 34
US-09-314-235-23
; Sequence 23, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT FILING DATE: 1999-05-18
; EARLIER FILING DATE: 1997-07-18
; EARLIER FILING DATE: 1994-06-02
; EARLIER FILING DATE: 1992-06-01
; EARLIER FILING DATE: 1991-01-17
; EARLIER FILING DATE: 1990-01-17
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-23

Query Match      81.1%; Score 1003.5; DB 4; Length 232;
Best Local Similarity 81.5%; Pred. No. 1e-94;
Matches 190; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTTG 60
DB 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTTG 60

QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTTPNKTCMYGGVTLHDNNRLT 120
DB 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTTPNKTCMYGGVTLHDNNRLT 120

QY 121 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 121 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180

QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLHDLYLTT 233
DB 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLHDLYLTT 233

RESULT 35
US-09-708-008B-23
; Sequence 23, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT FILING DATE: 2000-11-08
; EARLIER FILING DATE: 1997-07-18
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-708-008B-23

Query Match      81.1%; Score 1003.5; DB 4; Length 232;
Best Local Similarity 81.5%; Pred. No. 1e-94;
Matches 190; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTTG 60
DB 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTTG 60

QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTTPNKTCMYGGVTLHDNNRLT 120
DB 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTTPNKTCMYGGVTLHDNNRLT 120

QY 121 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 121 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180

QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLHDLYLTT 233
DB 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLHDLYLTT 233
```

Db 1 SEKSEINEKDLRKSELOQTALGNLKIYYINEKAKTENKESHQFL-HTILFKGFFTD 59
Qy 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
Db 60 HSWYNDLLVDFDSKDIYDKYKGVLDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 119
Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 120 EEKVPINLWIDGKQNTVPLETVTKNKVTVQELDPOARRYLOEKYNLYNSDVPDGGKVQ 179
Qy 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNKTINSENHLHDLYLVT 233
Db 180 RGLIVFHTSTEPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHMDIYLYTS 232

RESULT 36
US-09-144-776B-2
; Sequence 2, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-144-776B-2

Query Match 80.8%; Score 1000; DB 3; Length 257;
Best Local Similarity 80.7%; Pred. No. 2.7e-94;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;
Qy 1 SEKSEINEKDLRKSELOQTALGNLKIYYINEKAKTENKESHQFLHTILFKGFFTG 60
Db 25 SEKSEINEKDLRKSELOQTALGNLKIYYINEKAKTENKESHQFLHTILFKGFFTD 84

Qy 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIYDKYKGVLDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQNTVPLETVTKNKVTVQELDPOARRYLOEKYNLYNSDVPDGGKVQ 204
Qy 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNKTINSENHLHDLYLVT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHMDIYLYTS 257

RESULT 37
US-08-882-431B-2
; Sequence 2, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431B-2

Query Match 80.8%; Score 1000; DB 4; Length 257;
Best Local Similarity 80.7%; Pred. No. 2.7e-94;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;
Qy 1 SEKSEINEKDLRKSELOQTALGNLKIYYINEKAKTENKESHQFLHTILFKGFFTG 60
Db 25 SEKSEINEKDLRKSELOQTALGNLKIYYINEKAKTENKESHQFLHTILFKGFFTD 84
Qy 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIYDKYKGVLDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180

Db 145 BEKKVPIINLWLDGKQNTVPLETVTKNKNVTVQELDLQARRYLQKYNLYNSDVPDGVKQ 204
QY 181 RGLIVFHSSEGSTSYDLFDAGQGYPTLLRIYRDNKTINSENHLDLYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGYNTLLRIYRDNKTINSENWHIDIYLYTS 257

RESULT 38
US-09-144-776B-4
; Sequence 4, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-144-776B-4

Query Match 80.5%; Score 996; DB 3; Length 233;
Best Local Similarity 80.6%; Pred. No. 6e-94;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKKSLEQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTH 61
Db 2 EKSEINEKDLRKKSLEQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTH 61
QY 62 PWNDDLVLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
Db 62 SWYNDDLVRFDSDKIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 122 EKKVPIINLWLDGKQNTVPLETVTKNKNVTVQELDLQARRYLQKYNLYNSDVPDGVKQ 181
Db 122 EKKVPIINLWLDGKQNTVPLETVTKNKNVTVQELDLQARRYLQKYNLYNSDVPDGVKQ 181
QY 182 GLIVFHSSEGSTSYDLFDAGQGYPTLLRIYRDNKTINSENHLDLYLTT 233
Db 182 GLIVFHSSEGSTSYDLFDAGQGYPTLLRIYRDNKTINSENHLDLYLTT 233
QY 182 GLIVFHSSEGSTSYDLFDAGQGYPTLLRIYRDNKTINSENHLDLYLTT 233

Db 182 GLIVFHTSTEPSVNYDLFGAQGYNTLLRIYRDNKTINSENWHIDIYLYTS 233

RESULT 39
US-08-882-431B-4
; Sequence 4, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431B-4

Query Match 80.5%; Score 996; DB 4; Length 233;
Best Local Similarity 80.6%; Pred. No. 6e-94;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKKSLEQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTH 61
Db 2 EKSEINEKDLRKKSLEQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTH 61
QY 62 PWNDDLVLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
Db 62 SWYNDDLVRFDSDKIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 122 EKKVPIINLWLDGKQNTVPLETVTKNKNVTVQELDLQARRYLQKYNLYNSDVPDGVKQ 181
Db 122 EKKVPIINLWLDGKQNTVPLETVTKNKNVTVQELDLQARRYLQKYNLYNSDVPDGVKQ 181
QY 182 GLIVFHSSEGSTSYDLFDAGQGYPTLLRIYRDNKTINSENHLDLYLTT 233
Db 182 GLIVFHSSEGSTSYDLFDAGQGYPTLLRIYRDNKTINSENHLDLYLTT 233
QY 182 GLIVFHSSEGSTSYDLFDAGQGYPTLLRIYRDNKTINSENHLDLYLTT 233

RESULT 40
US-09-350-841A-1599

```
; Sequence 1599, Application US/09350841A
; Patent No. 6750008
; GENERAL INFORMATION:
; APPLICANT: Jefe, Peter;
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
; FILE REFERENCE: 7872-066-999
; CURRENT APPLICATION NUMBER: US/09/350,841A
; NUMBER OF SEQ ID NOS: 1946
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1599
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-350-841A-1599

Query Match      74.8%; Score 926.5; DB 4; Length 252;
Best Local Similarity 79.1%; Pred. No. 8.9e-87;
Matches 185; Conservative 16; Mismatches 26; Indels 7; Gaps 6;

Qy 1 SEKSEETNEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLKGPFTG 60
Db 25 SEKSEETNEKDLRKSELQGTALGNLRQIYYNEKAKTENKESHQDFLOHTLPKGFPTD 84
Qy 61 HPWYNDLLVLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSK-IVDKY--KKCD-YGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 140
Qy 121 BEKVPINLWIDGQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 141 BEKVPINLWIDGQNTVPLETAKTKNVTVOELD-QARRYLOEK-NLYNSDVFQGVQ 198
Qy 181 RGLVPHSSEGSTVSYDLFDA-QCGYPTLRIYRDNKTINSENHLHDLYLYTT 233
Db 199 RGLVPHSTPEFSVNYDLFGAGQGYSTNLLRIYRDNKTINSENHHDLYLYTS 252

RESULT 41
US-08-896-933-25
; Sequence 25, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-25

Query Match      53.1%; Score 657; DB 3; Length 228;
Best Local Similarity 55.6%; Pred. No. 3.2e-59;
Matches 125; Conservative 33; Mismatches 67; Indels 0; Gaps 0;

Qy 7 INEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLKGPFTGHPWYND 66
Db 2 VKEKELHKKSELSTALNNMKHSYADKNPIIGENKSTGDOFLENTLLYKFFTLINPFD 61
Qy 67 LLDVLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLTEKKVP 126
Db 62 LLINFSKEMAQHFKNVDVPIRYSINCYGGEIDRTACTYGGVTPHEGKNLKERKKIP 121
Qy 127 INLWIDGQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQGLIVF 186
Db 122 INLWINGVQKEVSLDKVQTDKKNVTVOELDLQARHYLQKDLKLYNNDTLGSKIQRGKIEF 181

RESULT 43
US-09-708-008B-25
; Sequence 25, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; EARLIER FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
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Db 122 INLWINGVQKEVSLDKVQTDKKNVTVOELDLQARHYLQKDLKLYNNDTLGSKIQRGKIEF 181
Qy 187 HSSEGSTVSYDLFDAQCGYPTLRIYRDNKTINSENHLHDLYLY 231
Db 182 DSSDGSKVSYDLFDVKGDFPEKQLRIYSDNKTLSLSTEHLDIYLY 226

RESULT 42
US-09-314-235-25
; Sequence 25, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; EARLIER FILING DATE: 1999-05-18
; EARLIER FILING DATE: 1997-07-18
; EARLIER FILING DATE: 1997-07-18
; EARLIER FILING DATE: 1994-06-02
; EARLIER FILING DATE: 1997/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER FILING DATE: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER FILING DATE: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER FILING DATE: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-25

Query Match      53.1%; Score 657; DB 3; Length 228;
Best Local Similarity 55.6%; Pred. No. 3.2e-59;
Matches 125; Conservative 33; Mismatches 67; Indels 0; Gaps 0;

Qy 7 INEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLKGPFTGHPWYND 66
Db 2 VKEKELHKKSELSTALNNMKHSYADKNPIIGENKSTGDOFLENTLLYKFFTLINPFD 61
Qy 67 LLDVLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLTEKKVP 126
Db 62 LLINFSKEMAQHFKNVDVPIRYSINCYGGEIDRTACTYGGVTPHEGKNLKERKKIP 121
Qy 127 INLWIDGQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQGLIVF 186
Db 122 INLWINGVQKEVSLDKVQTDKKNVTVOELDLQARHYLQKDLKLYNNDTLGSKIQRGKIEF 181

RESULT 43
US-09-708-008B-25
; Sequence 25, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; EARLIER FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
```

PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Charles H. Harris
 REGISTRATION NUMBER: 34,616
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 619-2065
 TELEFAX: (301) 619-7714
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 82
 TYPE: Amino Acid
 STRANDEDNESS: Unknown
 TOPOLOGY: Unknown
 MOLECULE TYPE: Peptide
 US-08-882-431B-19
 Query Match: 36.9%; Score 457; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 2.3e-39;
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 Qy 43 SDDQFLENTLLFKGFFTHPWYNLLVDLGSKDATNKYKGKKVDLYGAYYGQCAGGTPN 102
 Db 1 SDDQFLENTLLFKGFFTHPWYNLLVDLGSKDATNKYKGKKVDLYGAYYGQCAGGTPN 60

Qy 103 KTACMYGGVTLHDNNRLTEKK 124
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 46

```

US-09-144-776B-17
; Sequence 17, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
;
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC - 504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Att'y)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
;

```

Query Match	32.2%	Score 399;	DB 3;	Length 82;
Best Local Similarity	86.6%	Pred. No. 2.1e-33;		
Matches 71;	Conservative	4;	Mismatches 7;	Indels 0;
Gaps	0;			

Qy	43 SDOFLENTLLFKGFFFTGHFWYNDLLVLSKDATNKYKGKKVDLYGAYGYQCAGTPN 102 - : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : - : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db	1 SHOFLQHTILFKGFFFTDSWYNLDLVDFOSKDIVKYKGKKVDLYGAYGYQCAGTPN 60

Qy	103	KTACMYGGVTLHDNNRLTEKK	124
Db	61	KTACMYGGVTLHDNNRLTEKK	82

RESULT 47

US-08-882-431B-17
; Sequence 17, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,

APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MMC -504 Scott Street MO
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
CLASSIFICATION:

Query Match	32.2%	Score	399	DB	4	Length	82
Best Local Similarity	86.6%	Pred. No.	2.1e-33				
Matches	71	Conservative	4	Mismatches	7	Indels	0
Gaps	0						

Qy	43	SDQFLENTLLFKGFFTHCHPWYNDLLVDLGSKQATNKYKGGKKVDLYGAYGYQACAGT	102
Db	1	SHDQFLQHTILFKGFFTHSWYNDLLVDPDSKQIVDKYKGGKKVDLYGAYGYQACAGT	60

Qy	103	KTACMYGGVTLHDNNRLTEKK	124
Db	61	KTACMYGGVTLHDNNRLTEKK	82

RESIT.T 48

```

US-08-446-918A-2
; Sequence 2, Application US/08446918A
; Patent No. 5705151
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Emslie, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,918A
FILING DATE: 18-MAY-1995
CLASSIFICATION: 552
ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-29
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-918A-2

Query Match 24.2%; Score 300; DB 1; Length 255;
Best Local Similarity 34.0%; Pred. No. 1.5e-22;
Matches 83; Conservative 46; Mismatches 97; Indels 18; Gaps 7;
QY 1 SEKSEINEKLRKSELOLNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 15 SMESQDPKPDDELHKSSKFTGLMENMKVLYDDNHVSAL-NVKSIDQFLYDFLIYSIKOTK 73
QY 61 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQC-----AGTTPNKTCMYGG 110
DB 74 LGNYDNVRVEFKNKOLADKYKYDVFGANYYYQCYFSKKTNDINSHQTDKREKTCMYGG 133
QY 111 VTLHDNNRLTEKKVPIINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLY 170
DB 134 VTEHNGNQDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLY 191
QY 171 NSDSFGGKVGRLIVFHSSEGSTVSVDLFDQAQGYPD--TLRIYRDNKNTINSENHLIDL 228
DB 192 EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKNQWDSKDVKIEV 248
QY 229 YLYT 232
DB 249 YLTT 252

RESULT 49
US-08-580-806-2
Sequence 2, Application US/08580806
Patent No. 5935568
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
APPLICANT: Elmelie, Robyn E.
APPLICANT: Potter, Terence A.
TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,806
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-580-806-2
Query Match 24.2%; Score 300; DB 2; Length 255;
Best Local Similarity 34.0%; Pred. No. 1.5e-22;
Matches 83; Conservative 46; Mismatches 97; Indels 18; Gaps 7;
QY 1 SEKSEINEKLRKSELOLNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 15 SMESQDPKPDDELHKSSKFTGLMENMKVLYDDNHVSAL-NVKSIDQFLYDFLIYSIKOTK 73
QY 61 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQC-----AGTTPNKTCMYGG 110
DB 74 LGNYDNVRVEFKNKOLADKYKYDVFGANYYYQCYFSKKTNDINSHQTDKREKTCMYGG 133
QY 111 VTLHDNNRLTEKKVPIINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLY 170
DB 134 VTEHNGNQDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLY 191
QY 171 NSDSFGGKVGRLIVFHSSEGSTVSVDLFDQAQGYPD--TLRIYRDNKNTINSENHLIDL 228
DB 192 EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKNQWDSKDVKIEV 248
QY 229 YLYT 232
DB 249 YLTT 252

RESULT 50
US-08-896-933-29
Sequence 29, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 29
LENGTH: 221
TYPE: PRT
ORGANISM: Streptococcus pyogenes
US-08-896-933-29
Query Match 23.9%; Score 296.5; DB 3; Length 221;
Best Local Similarity 35.6%; Pred. No. 2.8e-22;
Matches 80; Conservative 42; Mismatches 84; Indels 19; Gaps 10;
QY 16 SELORNAL-SNLRQIYY-YNEKAIT-ENKESDDOFLNTLLFKGFFTGHPWYNLLVDLG 72
DB 7 SQRHSSLVKNLQNIYFLVEGDPVTHENVKSVDDQLSHDLIYN--VSGPNYDKLTCLK 63
QY 73 SKDATNKYKGVLDLYGAYGYQC-AGTTPNKTCMYGGVTLHDNNRLTEKKVPIINLWI 131
DB 64 NQEMATLFDKKNVDIYGVYHLYCYLCENASACIYGGVTHNEGHNLHLEPKKIVVKVSI 123
QY 132 DGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGELNSDSFGGKVGRLIVFHSSE 191

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Db 124 DGIO-SLSFD-IETNKKMVTAEQELDYKVRKYLTDNKKQLYTNGP--SKYETGYIKFIPKPK 179
Qy 192 STVSVDLFD----AQGOYPTDLLRIYRDNKTINSENHLIDLVLTY 232
Db 180 ESFWFDLPEPEFTQSKY----LMYKDNETLDSNTSQIEVLTY 220

RESULT 51
US-09-314-235-29
; Sequence 29, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; EARLIER FILING DATE: 1999-05-18
; EARLIER FILING DATE: 1997-07-18
; EARLIER FILING DATE: 1992-06-01
; EARLIER FILING DATE: 1994-06-02
; EARLIER FILING DATE: 1990-01-17
; EARLIER FILING DATE: 1990-01-17
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-29

Query Match 23.9%; Score 296.5; DB 3; Length 221;
Best Local Similarity 35.6%; Pred. No. 2.8e-22;
Matches 80; Conservative 42; Mismatches 84; Indels 19; Gaps 10;

Qy 16 SELQNAL-SNLROIYY-YNEKAIT-ENKESDDQFLENTLFLKGFFTGHPWYNDLLVDLG 72
Db 7 SQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLLSDLIYN--VSGPNYDKLKTLEK 63

Qy 73 SKDATNKYKGVLDLYGAYGYQC-AGGTPNKTACMGVTLHDNNRLTEKKVPINLWI 131
Db 64 NOEMATLFDKKNVDIYGVYVHLCYLCSNAERSACIYGGVTNHEGNHLEIPKKIWKVSI 123

Qy 132 DGKQTTVPIDKVTSSKEVTVOELDLOARHYLHGKFGLYNSDSFGGKVORGLIVPHSSEG 191
Db 124 DGIO-SLSFD-IETNKKMVTAEQELDYKVRKYLTDNKKQLYTNGP--SKYETGYIKFIPKPK 179

Qy 192 STVSVDLFD----AQGOYPTDLLRIYRDNKTINSENHLIDLVLTY 232
Db 180 ESFWFDLPEPEFTQSKY----LMYKDNETLDSNTSQIEVLTY 220

RESULT 52
US-09-314-235-29
; Sequence 29, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; EARLIER FILING DATE: 1999-05-18
; EARLIER FILING DATE: 1997-07-18
; EARLIER FILING DATE: 1992-06-01
; EARLIER FILING DATE: 1994-06-02
; EARLIER FILING DATE: 1990-01-17
; EARLIER FILING DATE: 1990-01-17
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-29

Query Match 23.9%; Score 296.5; DB 3; Length 221;
Best Local Similarity 35.6%; Pred. No. 2.8e-22;
Matches 80; Conservative 42; Mismatches 84; Indels 19; Gaps 10;

Qy 16 SELQNAL-SNLROIYY-YNEKAIT-ENKESDDQFLENTLFLKGFFTGHPWYNDLLVDLG 72
Db 7 SQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLLSDLIYN--VSGPNYDKLKTLEK 63

Qy 73 SKDATNKYKGVLDLYGAYGYQC-AGGTPNKTACMGVTLHDNNRLTEKKVPINLWI 131
Db 64 NOEMATLFDKKNVDIYGVYVHLCYLCSNAERSACIYGGVTNHEGNHLEIPKKIWKVSI 123

Qy 132 DGKQTTVPIDKVTSSKEVTVOELDLOARHYLHGKFGLYNSDSFGGKVORGLIVPHSSEG 191
Db 124 DGIO-SLSFD-IETNKKMVTAEQELDYKVRKYLTDNKKQLYTNGP--SKYETGYIKFIPKPK 179

Qy 192 STVSVDLFD----AQGOYPTDLLRIYRDNKTINSENHLIDLVLTY 232
Db 180 ESFWFDLPEPEFTQSKY----LMYKDNETLDSNTSQIEVLTY 220

RESULT 53
US-08-973-391C-13
; Sequence 13, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973.391C
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 13
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391C-13

Query Match 23.8%; Score 294.5; DB 4; Length 251;
Best Local Similarity 34.2%; Pred. No. 5.4e-22;
Matches 81; Conservative 45; Mismatches 92; Indels 19; Gaps 10;

Qy 4 SEINEKDLRKSELQNAL-SNLROIYY-YNEKAIT-ENKESDDQFLENTLFLKGFPTG 60
Db 25 SQEVFAQQDDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLLSDLIYN--VS 81

Qy 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQC-AGGTPNKTACMGVTLHDNNRL 119
Db 82 GPNYDKLKTLEKQEMATLFDKKNVDIYGVYVHLCYLCSNAERSACIYGGVTNHEGNH 141

Qy 120 TEKKVPINLWIDGQTTVPIDKVTSSKEVTVOELDLOARHYLHGKFGLYNSDSFGGKV 179
Db 142 EIPKKIWKVSIIDGQ-SLSFD-IETNKKMVTAEQELDYKVRKYLTDNKKQLYTNGP--SKY 197

Qy 180 QRLGIVPHSSEGSTVSVDLFD----AQGOYPTDLLRIYRDNKTINSENHLIDLVLTY 232
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Db 124 DGIO-SLSFD-IETNKKMVTAEQELDYKVRKYLTDNKKQLYTNGP--SKYETGYIKFIPKPK 179
Qy 192 STVSVDLFD----AQGOYPTDLLRIYRDNKTINSENHLIDLVLTY 232
Db 180 ESFWFDLPEPEFTQSKY----LMYKDNETLDSNTSQIEVLTY 220

RESULT 51
US-09-314-235-29
; Sequence 29, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; EARLIER FILING DATE: 1999-05-18
; EARLIER FILING DATE: 1997-07-18
; EARLIER FILING DATE: 1992-06-01
; EARLIER FILING DATE: 1994-06-02
; EARLIER FILING DATE: 1990-01-17
; EARLIER FILING DATE: 1990-01-17
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-29

Query Match 23.9%; Score 296.5; DB 3; Length 221;
Best Local Similarity 35.6%; Pred. No. 2.8e-22;
Matches 80; Conservative 42; Mismatches 84; Indels 19; Gaps 10;

Qy 16 SELQNAL-SNLROIYY-YNEKAIT-ENKESDDQFLENTLFLKGFFTGHPWYNDLLVDLG 72
Db 7 SQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLLSDLIYN--VSGPNYDKLKTLEK 63

Qy 73 SKDATNKYKGVLDLYGAYGYQC-AGGTPNKTACMGVTLHDNNRLTEKKVPINLWI 131
Db 64 NOEMATLFDKKNVDIYGVYVHLCYLCSNAERSACIYGGVTNHEGNHLEIPKKIWKVSI 123

Qy 132 DGKQTTVPIDKVTSSKEVTVOELDLOARHYLHGKFGLYNSDSFGGKVORGLIVPHSSEG 191
Db 124 DGIO-SLSFD-IETNKKMVTAEQELDYKVRKYLTDNKKQLYTNGP--SKYETGYIKFIPKPK 179

Qy 192 STVSVDLFD----AQGOYPTDLLRIYRDNKTINSENHLIDLVLTY 232
Db 180 ESFWFDLPEPEFTQSKY----LMYKDNETLDSNTSQIEVLTY 220

RESULT 52
US-09-708-008B-29
; Sequence 29, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
```


Db 198 ETGYIKFIPKNKESFWDFPEPEFTQSKY-----LMIYKDNELTDSNTSQIEVLYLT 250

RESULT 54
US-09-144-776B-6
; Sequence 6, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MMC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Att'y)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-144-776B-6

Query Match 23.7%; Score 293.5; DB 3; Length 266;
Best Local Similarity 32.8%; Pred. No. 7.4e-22;
Matches 80; Conservative 45; Mismatches 100; Indels 19; Gaps 7;
QY 1 SEKSEINEKDLRKXSELRNALSRLQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
Db 27 AESQPPKDPDLHKSKF--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTK 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQC-----AGGTPNKTCMYGG 110
Db 85 LGDYDNVRVEFKNKLADKYKDYVDVFGANYYYCYFVKKTNDINSHQTDKRTCMYGG 144
QY 111 VTLDHNNRLTEEEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLY 170
Db 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSPD-VQTNKKKVTAGELDYLTRHYLVKNKCLY 202
QY 171 NSDSFGGKVGQGLIVPHSSGSGTVSYDLFDAQOQ--YPTDLLRIYRDNKKTINSENHLIDL 228
Db 203 EFN--SPYETGYIKFTIENENS-FWYDMPAPGDKFAQSKYLMYNDNKNMVDKVKIEV 259
QY 229 YLYT 232

Db 260 YLYT 263
RESULT 55
US-08-882-431B-6
; Sequence 6, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MMC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Att'y)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431B-6

Query Match 23.7%; Score 293.5; DB 4; Length 266;
Best Local Similarity 32.8%; Pred. No. 7.4e-22;
Matches 80; Conservative 45; Mismatches 100; Indels 19; Gaps 7;
QY 1 SEKSEINEKDLRKXSELRNALSRLQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
Db 27 AESQPPKDPDLHKSKF--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTK 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQC-----AGGTPNKTCMYGG 110
Db 85 LGDYDNVRVEFKNKLADKYKDYVDVFGANYYYCYFVKKTNDINSHQTDKRTCMYGG 144
QY 111 VTLDHNNRLTEEEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLY 170
Db 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSPD-VQTNKKKVTAGELDYLTRHYLVKNKCLY 202
QY 171 NSDSFGGKVGQGLIVPHSSGSGTVSYDLFDAQOQ--YPTDLLRIYRDNKKTINSENHLIDL 228
Db 203 EFN--SPYETGYIKFTIENENS-FWYDMPAPGDKFAQSKYLMYNDNKNMVDKVKIEV 259
QY 229 YLYT 232
Db 260 YLYT 263

```
RESULT 56
US-08-896-933-26
; Sequence 26, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-08-896-933-26

Query Match      23.6%; Score 292.5; DB 3; Length 239;
Best Local Similarity 34.0%; Pred. No. 8e-22;
Matches 82; Conservative 44; Mismatches 96; Indels 19; Gaps 8;

QY 2 EKSEINEKDLRKXSELORNALSNLRIQIYYNEKAITENKESDDOFLNTLLFKGFFTGH 61
DB 1 ESQDPKPELHKSKF-TGLMNMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWYNDLLVGLGSKDATNKYKGKVDLYGAYGYQC-----AGGTPNKTCMYGGV 111
DB 59 GYDNRVVEFNKDLADKKYKVDVFGANYYYCYCFSKKNTDINSHTQDRKTCMYGGV 118
QY 112 TLHDNNRLTEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYN 171
DB 119 TEHNGNQLDKYRSLTRVRFEDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLYE 176
QY 172 SDSFGKGVQRLIVPHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENLIHDLY 229
DB 177 FNN--SPYETGYIKFIENENS-FWYDLMPAPGDKFDQSKYLMYNDNKNKVDKVKIEVY 233
QY 230 L 230
DB 234 L 234

RESULT 57
US-09-314-235-26
; Sequence 26, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0

Query Match      23.6%; Score 292.5; DB 3; Length 239;
Best Local Similarity 34.0%; Pred. No. 8e-22;
Matches 82; Conservative 44; Mismatches 96; Indels 19; Gaps 8;

QY 2 EKSEINEKDLRKXSELORNALSNLRIQIYYNEKAITENKESDDOFLNTLLFKGFFTGH 61
DB 1 ESQDPKPELHKSKF-TGLMNMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWYNDLLVGLGSKDATNKYKGKVDLYGAYGYQC-----AGGTPNKTCMYGGV 111
DB 59 GYDNRVVEFNKDLADKKYKVDVFGANYYYCYCFSKKNTDINSHTQDRKTCMYGGV 118
QY 112 TLHDNNRLTEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYN 171
DB 119 TEHNGNQLDKYRSLTRVRFEDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLYE 176
QY 172 SDSFGKGVQRLIVPHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENLIHDLY 229
DB 177 FNN--SPYETGYIKFIENENS-FWYDLMPAPGDKFDQSKYLMYNDNKNKVDKVKIEVY 233
QY 230 L 230
DB 234 L 234

RESULT 58
US-09-708-008B-26
; Sequence 26, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-09-708-008B-26

Query Match      23.6%; Score 292.5; DB 4; Length 239;
Best Local Similarity 34.0%; Pred. No. 8e-22;
Matches 82; Conservative 44; Mismatches 96; Indels 19; Gaps 8;

QY 2 EKSEINEKDLRKXSELORNALSNLRIQIYYNEKAITENKESDDOFLNTLLFKGFFTGH 61
DB 1 ESQDPKPELHKSKF-TGLMNMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWYNDLLVGLGSKDATNKYKGKVDLYGAYGYQC-----AGGTPNKTCMYGGV 111
DB 59 GYDNRVVEFNKDLADKKYKVDVFGANYYYCYCFSKKNTDINSHTQDRKTCMYGGV 118
QY 112 TLHDNNRLTEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYN 171
DB 119 TEHNGNQLDKYRSLTRVRFEDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLYE 176
QY 172 SDSFGKGVQRLIVPHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENLIHDLY 229
DB 177 FNN--SPYETGYIKFIENENS-FWYDLMPAPGDKFDQSKYLMYNDNKNKVDKVKIEVY 233
QY 230 L 230
DB 234 L 234
```

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QY 230 L 230
|
Db 234 L 234

RESULT 59
US-09-414-276-8
; Sequence 8, Application US/09414276
; Patent No. 6392121
; GENERAL INFORMATION:
; APPLICANT: Mason, Hugh
; APPLICANT: Palmer, Kenneth
; APPLICANT: Hefferon, Kathleen
; APPLICANT: Mor, Taafir
; APPLICANT: Arntzen, Charles
; TITLE OF INVENTION: Gemini Virus Vectors for Gene Expression in Plants
; FILE REFERENCE: 4868/84453
; CURRENT APPLICATION NUMBER: US/09/414,276
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; LENGTH: 266
; TYPE: PRT
; ORGANISM: bean yellow dwarf virus
US-09-414-276-8

Query Match 23.6%; Score 292.5; DB 3; Length 266;
Best Local Similarity 33.2%; Pred. No. 9.4e-22;
Matches 81; Conservative 47; Mismatches 97; Indels 19; Gaps 8;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 27 AESQDPKPELHKSCKP-TGLMENKVLDDNHVSAT-NVKSIDQSLYFDLIYSIKDTK 84
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 HPWYNDLLVLDGSKATNKYKGGKVDLYGAYGYQC-----AGTTPNKTAQMYGG 110
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 85 LGNYDNVRVEFNKDLADKDKYVDVFGANYYQCYFSKKTNDINSHQTDKRTKTCMYGG 144
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 111 VTLHNNRLTEKKVPINLWIDGKQTTVIDKVKTSKKEVTVOELDLQARHYLHGKFGLY 170
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAEGLDYLTRHYLVKNNKKLY 202
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 171 NSDSFGKVGQGLIVFHSSEGSTVSYVDLFDAGQOYED--TLRIRYRDNKTINSENHIDL 228
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 203 EFN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKWDSKVKIEV 259
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 229 YLYT 232
|
Db 260 YLTT 263

RESULT 60
US-08-973-391C-14
; Sequence 14, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14

; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391C-14

Query Match 23.5%; Score 291.5; DB 4; Length 221;
Best Local Similarity 35.1%; Pred. No. 9.1e-22;
Matches 79; Conservative 42; Mismatches 85; Indels 19; Gaps 10;

QY 16 SELQNAL-SNLRQIYY-YNKAIT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVDIG 72
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 SOLHSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHHLYN---VSGPNYDKLKLTELK 63
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 73 SKDATNKYKGGKVDLYGAYGYQC-AGTTPNKTAQMYGVTLHNNRLTEKKVPINLWI 131
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 NQEWATLFDKRNVDIYGVYHLCYLCENABRSACIYGGVTNHEGNHLEIPKKIVVKVSI 123
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 132 DGKQTTVIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHSSEG 191
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 124 DGIQ-SLSFD-IETNKKWATAQELDYKVKYLTDNKQLYTNGP--SKYETGYIKFIPKKN 179
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 STVSYDLEF---AQOYQPDTLRLRIYRDNKTINSENHIDLXYLT 232
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 180 ESFWEDEFFPEFTQSKY----LMIYKDNETLDSNTSQIEVYLT 220
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 61
US-09-144-776B-16
; Sequence 16, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MPMC -504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
```


Qy 69 VDLGSKDATNKYKGVLDLYGAYGYOCAGG-----TPNKTACMYGGVTLHDNR 118
Db 66 VEFKNKDLADKYDKYVDVFGANAYYQCAFSSKKTNDINSHQTDKRTKTCMYGGVTEHNGNQ 125
Qy 119 LTEEEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGK 178
Db 126 LDKYRSITVRVPEDGK-NLLSFD-VQTNKKVTAQELDYLTRHYLVKKNKLYEFPN--SP 181
Qy 179 VORGLIVFHSSEGSVSYDLFPAQOQYD--TLRIYRDNKTINSNLHIDLYLT 232
Db 182 YETGVYKFIENENS-FWYDMMPAPGDKFDQSKYLMYNDNKNWDSKDVKIEVLT 236

RESULT 64
US-08-882-431B-10
; Sequence 10, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-10

Query Match 23.3%; Score 288.5; DB 4; Length 239;
Best Local Similarity 33.9%; Pred. No. 2.1e-21;
Matches 80; Conservative 45; Mismatches 88; Indels 23; Gaps 8;

Qy 14 KXSELORNA-----LSNLRIQIYYNEKAITENKESDDQPLENTLLFKGFTGHPWNLL 68
Db 7 KPDELHKSKFTGLMENMKVLYDDNHVSAI-NVKSIDQFRYFDLIYSIKDTKLGNYDNVR 65
Qy 69 VDLGSKDATNKYKGVLDLYGAYGYOCAGG-----TPNKTACMYGGVTLHDNR 118
Db 66 VEFKNKDLADKYDKYVDVFGANAYYQCAFSSKKTNDINSHQTDKRTKTCMYGGVTEHNGNQ 125
Qy 119 LTEEEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGK 178

Db 126 LDKYRSITVRVPEDGK-NLLSFD-VQTNKKVTAQELDYLTRHYLVKKNKLYEFPN--SP 181
Qy 179 VORGLIVFHSSEGSVSYDLFPAQOQYD--TLRIYRDNKTINSNLHIDLYLT 232
Db 182 YETGVYKFIENENS-FWYDMMPAPGDKFDQSKYLMYNDNKNWDSKDVKIEVLT 236

RESULT 65
US-09-144-776B-8
; Sequence 8, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MMC -504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-144-776B-8

Query Match 22.8%; Score 282.5; DB 3; Length 266;
Best Local Similarity 32.8%; Pred. No. 1e-20;
Matches 80; Conservative 46; Mismatches 99; Indels 19; Gaps 8;

Qy 1 SKSSEINEKDLRKXSEIQORNLALNRQIYYNEKAITENKESDDQPLENTLLFKGFTG 60
Db 27 ABSQDPKPDLELHKSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFRYFDLIYSIKDTK 84
Qy 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYOCAGG-----TPNKTACMYGG 110
Db 85 LGNYDNVRVFEKKNKDLADKYDKYVDVFGANAYYQCAFSSKKTNDINSHQTDKRTKTCMYG 144
Qy 111 VTLHDNRNLTEEEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFG 170
Db 145 VTEHNGNQLDKYRSITVRVPEDGK-NLLSFD-VQYNKKVTAQELDYLTRHYLVKKNKLY 202

Qy 171 NSDSFGGKVGRLIVFHSSEGSTVSVDLFDAGQGYPD--TLIRIYRONKNTINSENHLIDL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAGDKFDQSKYLMYNDNMWVDSKDVKIEV 259
Qy 229 YLYT 232
Db 260 YLTT 263

RESULT 66
US-08-882-431B-8
; Sequence 8, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-8

Query Match 22.8%; Score 282.5; DB 4; Length 266;
Best Local Similarity 32.8%; Pred. No. 1e-20; 99; Indels 19; Gaps 8;
Matches 80; Conservative 46; Mismatches 99; Indels 19; Gaps 8;
Qy 1 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFTG 60
Db 27 AESQDPKPDLELHKSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFRYFDLIYSIKDTK 84
Qy 61 HPWYNDLLVGLSGDATNKYKGVLDLYGAYGYQCAGG-----TENKTACMYGG 110
Db 85 LGNYDNRVRFKNDLADKYDKYDVFEGANAYYQCAFSEKKTNDINSHQTDKRTKCYGG 144
Qy 111 VTLDHNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQBELDQARHYLHGKFGLY 170
Db 145 VTEHNGQLDKVRSITRVFDEGK-NLLSFD-VQYNNKKVTAQELDYLTRHYLVNKKLY 202
Qy 171 NSDSFGGKVGRLIVFHSSEGSTVSVDLFDAGQGYPD--TLIRIYRONKNTINSENHLIDL 228

Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAGDKFDQSKYLMYNDNMWVDSKDVKIEV 259
Qy 229 YLYT 232
Db 260 YLTT 263
RESULT 67
US-08-896-933-28
; Sequence 28, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-28
Query Match 22.7%; Score 281.5; DB 3; Length 238;
Best Local Similarity 32.5%; Pred. No. 1.1e-20;
Matches 76; Conservative 47; Mismatches 92; Indels 19; Gaps 9;
Qy 11 DLRKXSELQNALSNLRQIYYNEKAITENK-ESDDQPLENTLLFKGFTGHPWYNDLLV 69
Db 9 ELHKSSBF-TGTMCNMK--LYDDHYVSATKVMVDKFLAHDLIYNTISDKKLKNYDKVK 65
Qy 70 DLGSKDATNKYKGVLDLYGAYGYQC-----AGTTPNKTCMYGGVTLHDNNRLTEE 122
Db 66 ELLNDELAKYKDEVVDVYGSYVYVNCYFSSKDNVGVTKGKTCMYGGITKEGHNFDNG 125
Qy 123 --KKVPINLWIDGKQTTVPIDKVKTSKEVTVQBELDQARHYLHGKFGLYNSDSFGK 180
Db 126 NLQNVLRVY-ENKRNITISFE-VQTDKKSQVTAQELDIKARNFLINKKLYSFNS--SPVE 181
Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPD--TLIRIYRONKNTINSENHLIDL 232
Db 182 TGYIKFIENNGNTFWYDLMPPAGDKFDQSKYLMYNDNMWVDSKSVKIEVHLTT 235

RESULT 68
US-09-314-235-28
; Sequence 28, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-28

Query Match      22.7%; Score 281.5; DB 3; Length 238;
Best Local Similarity 32.5%; Pred. No. 1.1e-20;
Matches 76; Conservative 47; Mismatches 92; Indels 19; Gaps 9;

QY 11 DLKKSSELQNALSNLRQIYYNEKAITENK-ESDDQFLENTLLPKGFTGHPWYNDLIV 69
Db 9 ELHKSSEP-TGTMGNNK--YLDDHYVSATKMSVDKFLAHLDIYINISDKLKNYDKVKT 65
QY 70 DLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCACMYGGVTLHNNRLTEE 122
Db 66 ELLNEDLAKKYDEVDVYGSNYVNCYFSSKDNVGVKVTGGKTCMYGGITKEGHNHFDNG 125
QY 123 --KKVPINLWDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
Db 126 NLQNVLRVY-ENKRNITISFE-VQTDKKSVTQAQELDIKARNFLINKNLYEFNS--SPVE 181
QY 181 RGLIVHSSGSGTVSYDLFDAQGYPD--TLRLIYRDNKTINSENHLIDLILYT 232
Db 182 TGYIKFIENNGNTFWYDLMPAPGDKFQSKYLMYNDNKTVDKSKVIEVHLTT 235

RESULT 69
US-09-708-008B-28
; Sequence 28, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-708-008B-28

Query Match      22.7%; Score 281.5; DB 4; Length 238;
Best Local Similarity 32.5%; Pred. No. 1.1e-20;
Matches 76; Conservative 47; Mismatches 92; Indels 19; Gaps 9;

QY 11 DLKKSSELQNALSNLRQIYYNEKAITENK-ESDDQFLENTLLPKGFTGHPWYNDLIV 69
Db 9 ELHKSSEP-TGTMGNNK--YLDDHYVSATKMSVDKFLAHLDIYINISDKLKNYDKVKT 65
QY 70 DLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCACMYGGVTLHNNRLTEE 122
Db 66 ELLNEDLAKKYDEVDVYGSNYVNCYFSSKDNVGVKVTGGKTCMYGGITKEGHNHFDNG 125
QY 123 --KKVPINLWDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
Db 126 NLQNVLRVY-ENKRNITISFE-VQTDKKSVTQAQELDIKARNFLINKNLYEFNS--SPVE 181
QY 181 RGLIVHSSGSGTVSYDLFDAQGYPD--TLRLIYRDNKTINSENHLIDLILYT 232
Db 182 TGYIKFIENNGNTFWYDLMPAPGDKFQSKYLMYNDNKTVDKSKVIEVHLTT 235

RESULT 70
US-09-314-235-27
; Sequence 27, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
US-08-896-933-27
; Sequence 27, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-27

Query Match      21.6%; Score 267.5; DB 3; Length 239;
Best Local Similarity 31.0%; Pred. No. 2.9e-19;
Matches 75; Conservative 49; Mismatches 101; Indels 17; Gaps 8;

QY 2 EKSEBINEKDLRKSELORNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTTGH 61
Db 1 BSQDPDTPDELHKASKF-TGLMENNKKVLYDDHYVSATKVK-SVDKFLAHLDIYINISDKKL 58
QY 62 PWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCACMYGGVTLH 114
Db 59 KNYDKVKTLELNEGLAKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGGKTCMYGGITKH 118
QY 115 DNNRLTEE--KKVPINLWDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNS 172
Db 119 EGNHEFDNGNLQNVLRVY-ENKRNITISFE-VQTDKKSVTQAQELDIKARNFLINKNLYEF 176
QY 173 DSFGKVGORGLIVHSSGSGTVSYDLFDAQGYPD--TLRLIYRDNKTINSENHLIDLIL 230
Db 177 NS--SPYETGYIKFIENNGNTFWYDLMPAPGDKFQSKYLMYNDNKTVDKSKVIEVHL 234
QY 231 YT 232
Db 235 TT 236

RESULT 71
US-09-314-235-27
; Sequence 27, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
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```
; ORGANISM: Staphylococcus aureas
US-09-314-235-27

Query Match      21.6%; Score 267.5; DB 3; Length 239;
Best Local Similarity 31.0%; Pred. No. 2.9e-19;
Matches 75; Conservative 49; Mismatches 101; Indels 17; Gaps 8;

Qy 2 EKSEINEKDLRKKSELQNALSNLRQIYYNNEKAITENKESDDQFLENTLLFKGFFTGH 61
Db 1 ESQDPTDELHKASKF-TGLMENMKVLYDDHYVSATKVK-SVDKFLAHDLIYNSDKKL 58
Qy 62 PWYNDLLVGLSGDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTKACMYGGT 114
Db 59 KNYDKVKTELLNEGLAKKYDEVVDVYGSNNYVNCYFSSKDNVKGVTGGTKCMYGGITKH 118
Qy 115 DNNRLTEE--KKVPINLWIDGKQTPVDIKVTKSKKVTVOELDQARHYLHGKFGLYNS 172
Db 119 EGNHFDNGNLQNVLRVY-ENKRWITISFE-VQTKKSVTAQELDIKARNFLINKNLYEF 176
Qy 173 DSFGKQVQGLIVFHSSEGSTSVSYDLFDAQOQYD--TLLRIYRDNKTINSNLHIDL 230
Db 177 NS--SPYETGYIKFIENNGNTFWIDLMPAGDKFDQSKYLMYNDNKTVDKSKVIEVHL 234
Qy 231 YT 232
Db 235 TT 236

RESULT 72
US-09-708-008B-27
; Sequence 27, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708.008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896.933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252.978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-09-708-008B-27

Query Match      21.6%; Score 267.5; DB 4; Length 239;
Best Local Similarity 31.0%; Pred. No. 2.9e-19;
Matches 75; Conservative 49; Mismatches 101; Indels 17; Gaps 8;

Qy 2 EKSEINEKDLRKKSELQNALSNLRQIYYNNEKAITENKESDDQFLENTLLFKGFFTGH 61
Db 1 ESQDPTDELHKASKF-TGLMENMKVLYDDHYVSATKVK-SVDKFLAHDLIYNSDKKL 58
Qy 62 PWYNDLLVGLSGDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTKACMYGGT 114
Db 59 KNYDKVKTELLNEGLAKKYDEVVDVYGSNNYVNCYFSSKDNVKGVTGGTKCMYGGITKH 118
Qy 115 DNNRLTEE--KKVPINLWIDGKQTPVDIKVTKSKKVTVOELDQARHYLHGKFGLYNS 172
Db 119 EGNHFDNGNLQNVLRVY-ENKRWITISFE-VQTKKSVTAQELDIKARNFLINKNLYEF 176
Qy 173 DSFGKQVQGLIVFHSSEGSTSVSYDLFDAQOQYD--TLLRIYRDNKTINSNLHIDL 230
Db 177 NS--SPYETGYIKFIENNGNTFWIDLMPAGDKFDQSKYLMYNDNKTVDKSKVIEVHL 234
Qy 231 YT 232
Db 235 TT 236
```

```
Db 235 TT 236

RESULT 73
US-08-896-933-21
; Sequence 21, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896.933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252.978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-08-896-933-21

Query Match      21.0%; Score 260.5; DB 3; Length 239;
Best Local Similarity 31.8%; Pred. No. 1.5e-18;
Matches 78; Conservative 47; Mismatches 97; Indels 23; Gaps 10;

Qy 2 EKSEINEKDLRKKSELQNALSNLRQIYYNNEKAITENKESDDQFLENTLLFKGFFTGH 61
Db 1 ESQDPTDELHKASKF--TGLMENMKVLYNDHVSAINVKISINEFFDLIYLSIKDTKL 58
Qy 62 PWYNDLLVGLSGDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTKACMYGG 110
Db 59 GNYDNVTRVEFKNDLADKYDKYDVDFGANY-YQCYFSKKTNNIDSHENTKRKT-CMYGG 116
Qy 111 VTLDHNNRLTE-EKKVPINLWIDGKQTPVDIKVTKSKKVTVOELDQARHYLHGKFG 169
Db 117 VTEHGNQLDKYRSITVRVPEDGK-NLLSPD-VQTNKKKVTABQDLYLTHYLVKNKL 174
Qy 170 YNDSFGKQVQGLIVFHSSEGSTSVSYDLFDAQOQYD--TLLRIYRDNKTINSNLH 227
Db 175 YEFNN--SPYETGYIKFIENENS-FWYDMPAPGNKFDQSKYLMYNDNKTVDKSKV 231
Qy 228 LYLYT 232
Db 232 VYLT 236

RESULT 74
US-09-314-235-21
; Sequence 21, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314.235
; CURRENT FILING DATE: 1999-03-18
; EARLIER APPLICATION NUMBER: 08/896.933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252.978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891.718
; EARLIER FILING DATE: 1992-08-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466.577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416.530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
```


Db 203 FNS--SFYETGYIKFIENNGNTFWYDMMAPGDKFQDOSKYLMTYNDKNTVDSKSVKIEVH 260
Qy 230 LYT 232
Db 261 LTT 263

RESULT 77
US-08-882-431B-14
; Sequence 14, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-14

Query Match 20.9%; Score 258.5; DB 4; Length 266;
Best Local Similarity 30.0%; Pred. No. 2.9e-18;
Matches 73; Conservative 51; Mismatches 102; Indels 17; Gaps 8;

Qy 1 SEKSEINEKDLRKKSELQNALSNLRQIYYNYNEKAITENKESDDQFLENTLLFKGFTG 60
Db 27 AESQPDPTPDELHKASKF-TGLMENMKVLYDDHYVVSATKVK-SVDKFRADLIYNSDKK 84
Qy 61 HPWYNDLLDGLSGDATNKYKGGKVDLYGAVYGOC-----AGGTENKTACMGVGYTL 113
Db 85 LKNYDKVKTETELLNEGLAKYKDEVDVYGSNYNYNCYFSSKDNVGVKVTGGKTCMYGGITK 144
Qy 114 HDNRLTTEE--KKVPINLIWDGQKTPPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
Db 145 HEGNHFDNGNLQNLIRVY-ENKRNITISFE-VQTDKKSVTQAQELDIKARNFLINKNLNLYE 202
Qy 172 SDSFGGKVQGLIIVPHSSEGSTVSVDLFDQAQGYPD--TLRIYRDNKTINSNLHIDL 229
Db 203 FNS--SFYETGYIKFIENNGNTFWYDMMAPGDKFQDOSKYLMTYNDKNTVDSKSVKIEVH 260

Qy 230 LYT 232
Db 261 LTT 263

RESULT 78
US-08-896-933-20
; Sequence 20, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-896-933-20

Query Match 19.8%; Score 245; DB 3; Length 220;
Best Local Similarity 30.7%; Pred. No. 5.3e-17;
Matches 70; Conservative 42; Mismatches 94; Indels 22; Gaps 9;

Qy 14 KKSLEQNALSNLRQIYYNYNEKA--IT-ENKESDDQFLENTLLFKGFTGHPWYNDLLVD 70
Db 5 KPSQLQRSNLVKTPIYIFFMRVTLVTHENVKSVVDQLLSHDLIYN---VSGPNYDKLAKTE 61
Qy 71 LGSKDATNKYKGGKVDLYGAVYGOC-AGGTPNKTACMGYGVTLHDNRLTTEEKKVPINL 129
Db 62 LKNQEMATLFDKKNVDIYGVVEYHLCYLCEAERSACLYGCVTNHEGNHLSIPKKIVVKV 121
Qy 130 WIDGKQT-TVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQGLIIVPHS 188
Db 122 SIDGIQSLSFDFIQIKNG----NCSRSYTVTKVYLTNKNQLYTNGP--SKYETGYIKPIP 175
Qy 189 SEGSTVSVDLFD----AQGQVPTLLRIYRDNKTINSNLHIDL 232
Db 176 KNKESFWDFPPEPEFTQSKY----LMYKDNETLDSNTSQIEVYLT 219

RESULT 79
US-09-314-235-20
; Sequence 20, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 3.0

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; SEQ ID NO 20
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-20

Query Match      19.8%; Score 245; DB 3; Length 220;
Best Local Similarity 30.7%; Pred. No. 5.3e-17;
Matches 70; Conservative 42; Mismatches 94; Indels 22; Gaps 9;

QY 14 KKSELORNALSNLRQIYYNEKA--IT-ENKESDDOFLNTLLFKGFTGHPWYNDLLVD 70
DB 5 KPSQLQSNLVKTFKIIYIPFMRVTLVTHENVKSDQLLSDHDIYN---VSGPNYDKLKTE 61
QY 71 LGSKDATNKYKGKVDLYGAYGYQC-AGGTENKACMYGGVTLHDNNRLTEKKVPINL 129
DB 62 LKQEMATLFDKKNVDIYGVVEYHLYCNCENASACLYGGVTNHEGNHLEIPKIVVKV 121
QY 130 WIDGKQT-TVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHS 188
DB 122 SIDGIQSLSFDEIQKNG---NCSRSIVTVRKYLTDNKLVTNGP--SKYETGYIKFIP 175
QY 189 SEGSTVSYDLFD-----AQQYPTLLRIYRDNKTINSENHLIDLYLT 232
DB 176 KKNESFWDFEPEPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 219

RESULT 80
US-09-708-008B-20
; Sequence 20, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-708-008B-20

Query Match      19.8%; Score 245; DB 4; Length 220;
Best Local Similarity 30.7%; Pred. No. 5.3e-17;
Matches 70; Conservative 42; Mismatches 94; Indels 22; Gaps 9;

QY 14 KKSELORNALSNLRQIYYNEKA--IT-ENKESDDOFLNTLLFKGFTGHPWYNDLLVD 70
DB 5 KPSQLQSNLVKTFKIIYIPFMRVTLVTHENVKSDQLLSDHDIYN---VSGPNYDKLKTE 61
QY 71 LGSKDATNKYKGKVDLYGAYGYQC-AGGTENKACMYGGVTLHDNNRLTEKKVPINL 129
DB 62 LKQEMATLFDKKNVDIYGVVEYHLYCNCENASACLYGGVTNHEGNHLEIPKIVVKV 121
QY 130 WIDGKQT-TVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHS 188
DB 122 SIDGIQSLSFDEIQKNG---NCSRSIVTVRKYLTDNKLVTNGP--SKYETGYIKFIP 175
QY 189 SEGSTVSYDLFD-----AQQYPTLLRIYRDNKTINSENHLIDLYLT 232
DB 176 KKNESFWDFEPEPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 219

RESULT 81
US-09-144-776B-18
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```
; Sequence 18, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MEMC -504 Scott Street
; MCWR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-144-776B-18

Query Match      17.4%; Score 215; DB 3; Length 82;
Best Local Similarity 51.2%; Pred. No. 1.5e-14;
Matches 41; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

QY 45 DOFLENTLLFKGFTGHPWYNDLLVDLGSKDATNKYKGKVDLYGAYGYQCAGGTENKT 104
DB 3 DOFLENTLLFKGFTGHPWYNDLLVDLGSKDATNKYKGKVDLYGAYGYQCAGGTENKT 62
QY 105 ACMYGGVTLHDNNRLTEKK 124
DB 63 ACTYGGVTPHEGNKLERKK 82

RESULT 82
US-08-882-431B-18
; Sequence 18, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
```

STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Att'y)

CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882.431B
FILING DATE: June 25, 1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris

REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:
LENGTH: 82
TYPE: Amino Acid

STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide

US-08-882-431B-18

Query Match 17.4%; Score 215; DB 4; Length 82;
Best Local Similarity 51.2%; Pred. No. 1.5e-14;
Matches 41; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

Qy 45 DQLENTLLFGFFGHPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYOCAGTPTNKT 104
Db 3 DQLENTLLYKFFDTDLINFDLLINFNSKEWAQHFKSNVDVPIRYSINCYGGEIDRT 62

Qy 105 ACMYGGVTLHDNNRLTERKK 124
Db 63 ACTYGGVTPHEGNKLKERKK 82

RESULT 83
US-08-220-378-1
Sequence 1, Application US/08220378
Patent No. 5545716

GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.

APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville
STATE: FL
COUNTRY: USA

ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220.378
FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,497

FILING DATE: 08-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-220-378-1

Query Match 15.4%; Score 191; DB 1; Length 45;
Best Local Similarity 86.7%; Pred. No. 1.8e-12;
Matches 39; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKXSELQNALNSLRQIYYYNKAITENKESDD 45
Db 1 SEKSEINEKDLRKXSELQGTALGNLQIYYYNKAKTENKESHD 45

RESULT 84
US-08-696-012-1
Sequence 1, Application US/08696012
Patent No. 5859207

GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.

APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville
STATE: FL
COUNTRY: USA

ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696.012
FILING DATE: 12-AUG-1996

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/220,378

FILING DATE: 29-MAR-1994
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992

CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid

STRANDEDNESS: single

APPLICANT: Gahr, Pamela J.
TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN C AND METHODS OF USE

Qy 193 TVSYDLFPA--QGQVPTLLRIYRDNKTINSNL-HIDLVL 230
Db 167 HEQIDLFSPNEGTRSDIFAK-YKDNRIINNMKNFSHFDIYL 206

RESULT 88

US-09-314-235-30
; Sequence 30, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-30

Query Match 14.7%; Score 181.5; DB 3; Length 208;
Best Local Similarity 27.1%; Pred. No. 1.6e-10;
Matches 60; Conservative 41; Mismatches 75; Indels 45; Gaps 11;
Qy 40 NKESDDQFLNTLLFKGFFTGHPW-YNDLLVDLGSKDA-----TNKYKGK----- 83
Db 1 DSKKDISNVKSDLLYA--YTITPYDKCRVNFSTHTLTIDTQYRGKDYIISSEMSYE 58
Qy 84 -----KVDLYGAVYGYQCAGGTGPNKTACMGVGTLLHDNNRLTEKKVPINLWIDGK 134
Db 59 ASQKFKRDDHVDVFGFLYILNSHTG-----EYIYGITPAQNNKNVH--KLLGNLFISGE 111
Qy 135 QTTVPIDKVTSSKEVTVQELDLQARHYLHGKFLYNSDS--FGGKVQRGVLIVFHSSEGS 192
Db 112 SQQNLNNKIILEKDIVTFQEIIDFKIRKYLMDNYKIYDATSPVVSGRIEIG-----TKDGK 166
Qy 193 TVSYDLFPA--QGQVPTLLRIYRDNKTINSNL-HIDLVL 230
Db 167 HEQIDLFSPNEGTRSDIFAK-YKDNRIINNMKNFSHFDIYL 206

RESULT 89

US-09-708-008B-30
; Sequence 30, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-708-008B-30
Query Match 14.7%; Score 181.5; DB 4; Length 208;
Best Local Similarity 27.1%; Pred. No. 1.6e-10;
Matches 60; Conservative 41; Mismatches 75; Indels 45; Gaps 11;
Qy 40 NKESDDQFLNTLLFKGFFTGHPW-YNDLLVDLGSKDA-----TNKYKGK----- 83
Db 1 DSKKDISNVKSDLLYA--YTITPYDKCRVNFSTHTLTIDTQYRGKDYIISSEMSYE 58
Qy 84 -----KVDLYGAVYGYQCAGGTGPNKTACMGVGTLLHDNNRLTEKKVPINLWIDGK 134
Db 59 ASQKFKRDDHVDVFGFLYILNSHTG-----EYIYGITPAQNNKNVH--KLLGNLFISGE 111
Qy 135 QTTVPIDKVTSSKEVTVQELDLQARHYLHGKFLYNSDS--FGGKVQRGVLIVFHSSEGS 192
Db 112 SQQNLNNKIILEKDIVTFQEIIDFKIRKYLMDNYKIYDATSPVVSGRIEIG-----TKDGK 166
Qy 193 TVSYDLFPA--QGQVPTLLRIYRDNKTINSNL-HIDLVL 230
Db 167 HEQIDLFSPNEGTRSDIFAK-YKDNRIINNMKNFSHFDIYL 206

RESULT 90

US-09-144-776B-20
; Sequence 20, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown

MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-144-776B-20

Query Match 11.1%; Score 137.5; DB 3; Length 89;
Best Local Similarity 39.1%; Pred. No. 1.5e-06;
Matches 34; Conservative 14; Mismatches 28; Indels 11; Gaps 2;

QY 43 SDDQPLENTLLFKGFTGHPWYNDLLVGLSKDATNKYKGVVLYGAYGYQC----- 96
DB 1 SIDQFLYFDLYISKDTKLGNDVNRVFEKKNLADKYDKYDVFGANY-YQCYFSKKT 59

QY 97 ----AGGTPNKTKACMYGGVTLHDNNRL 119
DB 60 NDINSHQTDKRTKCMYGGVTEHNGNQL 86

RESULT 91
US-08-882-431B-20
; Sequence 20, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MPMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/0882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-20

Query Match 11.1%; Score 137.5; DB 4; Length 89;
Best Local Similarity 39.1%; Pred. No. 1.5e-06;
Matches 34; Conservative 14; Mismatches 28; Indels 11; Gaps 2;

QY 43 SDDQPLENTLLFKGFTGHPWYNDLLVGLSKDATNKYKGVVLYGAYGYQC----- 96
DB 1 SIDQFLYFDLYISKDTKLGNDVNRVFEKKNLADKYDKYDVFGANY-YQCYFSKKT 59

QY 97 ----AGGTPNKTKACMYGGVTLHDNNRL 119
DB 60 NDINSHQTDKRTKCMYGGVTEHNGNQL 86

Db 60 NDINSHQTDKRTKCMYGGVTEHNGNQL 86

RESULT 92
US-08-220-378-2
; Sequence 2, Application US/08220378
; Patent No. 5545716
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Griggs, Nathan D.
; TITLE OF INVENTION: Superantigen Agonist and Antagonist
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/220,378
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,497
; FILING DATE: 08-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UFI26.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-220-378-2

Query Match 10.4%; Score 129; DB 1; Length 28;
Best Local Similarity 78.6%; Pred. No. 2e-06;
Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 39 ENKESDDQPLENTLLFKGFTGHPWYND 66
DB 1 ENKESDDQPLENTLLFKGFTGHPWYND 28

RESULT 93
US-08-696-012-2
; Sequence 2, Application US/08696012
; Patent No. 5859207
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Griggs, Nathan D.
; TITLE OF INVENTION: Superantigen Agonist and Antagonist
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville

```
/ STATE: FL
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/696,012
/ FILING DATE: 12-AUG-1996
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/220,378
/ FILING DATE: 29-MAR-1994
/ APPLICATION NUMBER: US 07/941,497
/ FILING DATE: 08-SEP-1992
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 31,794
/ REFERENCE/DOCKET NUMBER: UF126.C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 904-375-8100
/ TELEFAX: 904-372-5800
/ INFORMATION FOR SEQ ID NO: 2:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-696-012-2

Query Match 10.4%; Score 129; DB 2; Length 28;
Best Local Similarity 78.6%; Pred. No. 2e-06;
Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 39 ENKESDDQFLENTLLFKGFTGHWPYND 66
Db 1 ENKESDQFLQHTILFRGFFTDHSHWYND 28

RESULT 94
US-08-838-413A-22
/ Sequence 22, Application US/08838413A
/ Patent No. 6075119
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: PEPTIDES USEFUL FOR
/ TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME
/ NUMBER OF SEQUENCES: 31
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORGAN & FINNEGAN
/ STREET: 345 PARK AVENUE
/ CITY: NEW YORK
/ STATE: NEW YORK
/ COUNTRY: USA
/ ZIP: 10154
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WORDPERFECT 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/838.413A
/ FILING DATE: 07-APR-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION: 536
```

```
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MORRY, MARY J.
/ REGISTRATION NUMBER: 34,398
/ REFERENCE/DOCKET NUMBER: 2016-4010
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)758-4800
/ TELEFAX: (212)751-6849
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 24
/ TYPE: AMINO ACID
/ STRANDEDNESS: UNKNOWN
/ TOPOLOGY: UNKNOWN
/ MOLECULE TYPE: PEPTIDE
/ US-08-838-413A-22

Query Match 10.3%; Score 127; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 KKEVTVOELDQARHYLHGKFGLY 170
Db 1 KKEVTVOELDQARHYLHGKFGLY 24

RESULT 95
US-08-220-378-5
/ Sequence 5, Application US/08220378
/ Patent No. 5545716
/ GENERAL INFORMATION:
/ APPLICANT: Johnson, Howard M.
/ APPLICANT: Pontzer, Carol H.
/ APPLICANT: Griggs, Nathan D.
/ TITLE OF INVENTION: Superantigen Agonist and Antagonist
/ TITLE OF INVENTION: Peptides
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Saliwanchik & Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: FL
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/220,378
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/941,497
/ FILING DATE: 08-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 31,794
/ REFERENCE/DOCKET NUMBER: UF126.C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 904-375-8100
/ TELEFAX: 904-372-5800
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 23 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-220-378-5

Query Match 10.2%; Score 126; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 NKTACMYGGVTLHDNNRLTEKK 124
   |||||
Db 1 NKTACMYGGVTLHDNNRLTEKK 23

RESULT 96
US-08-696-012-5
; Sequence 5, Application US/08696012
; Patent No. 5859207
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Griggs, Nathan D.
; TITLE OF INVENTION: Superantigen Agonist and Antagonist
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,012
; FILING DATE: 12-AUG-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/220,378
; FILING DATE: 29-MAR-1994
; APPLICATION NUMBER: US 07/941,497
; FILING DATE: 08-SEP-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF126.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-696-012-5
Query Match 10.2%; Score 126; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 NKTACMYGGVTLHDNNRLTEKK 124
   |||||
Db 1 NKTACMYGGVTLHDNNRLTEKK 23

RESULT 97
US-08-220-378-6
; Sequence 6, Application US/08220378
; Patent No. 5545716
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Griggs, Nathan D.
; TITLE OF INVENTION: Superantigen Agonist and Antagonist
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,012
; FILING DATE: 12-AUG-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/220,378
; FILING DATE: 29-MAR-1994
; APPLICATION NUMBER: US 07/941,497
; FILING DATE: 08-SEP-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF126.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-696-012-5
Query Match 10.0%; Score 124; DB 1; Length 29;
Best Local Similarity 78.6%; Pred. No. 7e-06;
Matches 22; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 121 BEKKVPINLWDGKQTTVPIDKVKTKK 148
   |||||
Db 1 BEKKVPINLWDGKQTTVPIDKVKTKK 28

RESULT 98
US-08-696-012-6
; Sequence 6, Application US/08696012
; Patent No. 5859207
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Griggs, Nathan D.
; TITLE OF INVENTION: Superantigen Agonist and Antagonist
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,012
; FILING DATE: 12-AUG-1996
```

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;
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/220,378
; FILING DATE: 29-MAR-1994
; APPLICATION NUMBER: US 07/941,497
; FILING DATE: 08-SEP-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UFI26.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-696-012-6

Query Match 10.0%; Score 124; DB 2; Length 29;
Best Local Similarity 78.6%; Pred. No. 7e-06;
Matches 22; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 121 BEKKVPINLWIDGQTTVPIDKVTSKK 148
Db 1 BEKKVPINLWIDGQNTVPLETVTNNK 28

RESULT 99
US-09-144-776B-24
; Sequence 24, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431B-24

Query Match 9.8%; Score 121; DB 4; Length 79;
Best Local Similarity 34.6%; Pred. No. 6.1e-05;
Matches 27; Conservative 15; Mismatches 32; Indels 4; Gaps 2;
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```
;
; LENGTH: 79
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
; US-09-144-776B-24

Query Match 9.8%; Score 121; DB 3; Length 79;
Best Local Similarity 34.6%; Pred. No. 6.1e-05;
Matches 27; Conservative 15; Mismatches 32; Indels 4; Gaps 2;

Qy 43 SDDQFLENTLLFKGFTTGHWPYNDLLVDLGSKDATNKYKGVLDLYGAYGYQC-AGGTP 101
Db 1 SVDQLSHDLIYN---VSGPNYDKLTTELKKNQENATLFDKKNVDIYGVEYVHLCYCENA 57
Qy 102 NKTACMYGGVTLHDNNEL 119
Db 58 ERSACIYGGVTNHEGNHL 75

RESULT 100
US-08-882-431B-24
; Sequence 24, Application US/0882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431B-24

Query Match 9.8%; Score 121; DB 4; Length 79;
Best Local Similarity 34.6%; Pred. No. 6.1e-05;
Matches 27; Conservative 15; Mismatches 32; Indels 4; Gaps 2;

Qy 43 SDDQFLENTLLFKGFTTGHWPYNDLLVDLGSKDATNKYKGVLDLYGAYGYQC-AGGTP 101
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
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Db 1 SVDQLLSDLIYN---VSGFNVDKLTTELKNOEMATLFDKXNVDIYGVVEYHLCYLCEA 57

Qy 102 NKTACWYGGVTLHDNNRL 119

Db :||:|||||:|
58 ERSACIYGGVTNHEGNHL 75

Search completed: July 26, 2005, 11:09:10
Job time : 28 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 10:57:03 ; Search time 72 Seconds
(without alignments)
1251.600 Million cell updates/sec

Title: US-09-900-766-7

Perfect score: 1238
Sequence: 1 SEKSEINEKLRKKSELQR.....RDNKTINSENLHLDLYLT 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : A_Geneseq_16Dec04:*

1: Genesecp1980s:*

2: Genesecp1990s:*

3: Genesecp2000s:*

4: Genesecp2001s:*

5: Genesecp2002s:*

6: Genesecp2003as:*

7: Genesecp2003bs:*

8: Genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1238	100.0	233	6	ABP58456 Staphyloc
2	1238	100.0	257	4	AAU14103
3	1238	100.0	257	6	ABO10268 S. aureus
4	1238	100.0	257	8	ADF89830 Staphyloc
5	1234	98.9	230	4	AAB67339
6	1222	98.7	245	2	AAW35374
7	1210	97.7	233	6	ABP58457
8	1202	97.1	245	2	AAW35375
9	1188	96.0	248	6	ABU79072 S. aureus
10	1188	96.0	248	7	ADF43296 Staphyloc
11	1179	95.2	230	2	AAW45012
12	1175	94.9	230	5	ABW76235
13	1156	93.4	230	2	AAW13204
14	1107	89.4	233	6	ABP58455
15	1107	89.4	672	6	ABP58454
16	1035	83.6	233	2	AAW13203
17	1023	82.6	233	6	ABP58458
18	1023	82.6	257	4	AAU14104
19	1023	82.6	257	6	ABO10269
20	1023	82.6	257	7	ADD44368
21	1023	82.6	257	8	ADH10956
22	1019	82.3	233	2	AAW06738
23	1019	82.3	233	8	ADI95318
24	1016	82.1	233	2	AAW35373
25	1016	82.1	233	4	AAB67338

99	292.5	23.6	266	3	AA92319	Plant-opt	172	250	20.2	209	8	ADG69998	Adg69998	Mutant St
100	291.5	23.5	266	7	ABU62453	S. aureus	173	250	20.2	209	8	ADG70011	Adg70011	Mutant St
101	290.5	23.5	239	5	ABB76237	Staphyloc	174	247.5	20.0	209	8	ADG69999	Adg69999	Mutant St
102	290.5	23.5	251	7	ABU62460	Streptoco	175	247.5	20.0	209	8	ADG70010	Adg70010	Mutant St
103	289.5	23.4	251	2	AAW59798	Amino aci	176	245.5	19.8	231	7	ADG64940	Adg64940	SEB pepti
104	289.5	23.4	251	2	AAW59781	Amino aci	177	245	19.8	250	6	ABU79074	Abu79074	S. pyogen
105	289.5	23.4	251	3	AA970109	Streptoco	178	245	19.8	250	7	ADF43300	Adf43300	Pyrogenic
106	289.5	23.4	251	5	ABB79508	Streptoco	179	239	19.3	209	8	ADF89845	Adf89845	Streptoco
107	289.5	23.4	251	6	ABU10088	Streptoco	180	232	18.7	258	5	ADP29565	Adp29565	Streptoco
108	289.5	23.4	251	7	ABU62331	Streptoco	181	220.5	17.8	240	8	ADF89826	Adf89826	Staphyloc
109	289.5	23.4	251	7	AAE37683	Streptoco	182	217	17.5	234	3	AA93742	Aay93742	Amino aci
110	289.5	23.4	266	3	AA954464	Amino aci	183	217	17.5	234	5	ADP29092	Adp29092	Streptoco
111	288.5	23.3	239	2	AA906253	Staphyloc	184	216	17.4	210	8	ADF89843	Adf89843	Streptoco
112	288.5	23.3	239	5	ABB79505	Staphyloc	185	215	17.4	82	6	ABU10090	Abu10090	Bacterial
113	288.5	23.3	239	6	ABU10085	Staphyloc	186	215	17.4	82	7	ABU62337	Abu62337	S. aureus
114	288.5	23.3	239	7	ABU62328	S. aureus	187	197	15.9	236	3	AA93743	Aay93743	Amino aci
115	288.5	23.3	239	7	AAE37680	Protein #	188	197	15.9	236	5	ABP29358	Abp29358	Streptoco
116	288.5	23.3	240	3	AA954465	Mutant St	189	197	15.9	236	8	ADF89844	Adf89844	Streptoco
117	288.5	23.3	240	6	ABG71369	Staphyloc	190	197	15.9	236	8	ADR83928	Adr83928	S. pyogen
118	287.5	23.2	239	2	AA906256	Staphyloc	191	193	15.6	232	5	ADP29143	Adp29143	Streptoco
119	287.5	23.2	239	3	AA970106	Mutant St	192	191	15.4	45	2	AAW04488	Aaw04488	Staphyloc
120	287.5	23.2	240	6	ABG71372	Staphyloc	193	191	15.4	45	2	AAW73917	Aaw73917	Staphyloc
121	287.5	23.2	266	7	ABU62454	S. aureus	194	185	14.9	234	8	ADF89841	Adf89841	Streptoco
122	285.5	23.1	239	2	AA906255	Staphyloc	195	183.5	14.8	235	2	AAW62788	Aaw62788	Mutant St
123	285.5	23.1	239	8	ADL14256	Modified	196	183.5	14.8	235	2	AAW62787	Aaw62787	Mutant St
124	285.5	23.1	240	6	ABG71371	Staphyloc	197	182.5	14.7	207	5	AAE25373	Aae25373	S. pyogen
125	285.5	23.1	266	8	ADF89828	Staphyloc	198	182.5	14.7	207	5	AAE25373	Aae25373	S. pyogen
126	284.5	23.0	251	2	AAW12149	Streptoco	199	181.5	14.7	207	5	AAE25364	Aae25364	Streptoco
127	284.5	23.0	251	2	AAW12152	Streptoco	200	181.5	14.7	208	2	AAE13210	Aae13210	Streptoco
128	284.5	23.0	266	7	ABU62452	S. aureus								
129	284.5	23.0	266	7	ABU62451	S. aureus								
130	283.5	22.9	239	2	AA906252	Staphyloc								
131	283.5	22.9	240	6	ABG71368	Staphyloc								
132	283	22.9	250	2	AAW12145	Streptoco								
133	282.5	22.8	266	5	ABB79504	Staphyloc								
134	282.5	22.8	266	6	ABU10084	Staphyloc								
135	282.5	22.8	266	7	ABU62327	S. aureus								
136	282.5	22.8	266	7	AAE37679	Protein #								
137	281.5	22.7	238	2	AAE37679	Staphyloc								
138	280.5	22.7	239	8	ADF89827	Staphyloc								
139	280	22.6	265	3	AA970104	Staphyloc								
140	279.5	22.6	238	4	AAAB67343	Staphyloc								
141	279.5	22.6	238	5	ABB76239	Staphyloc								
142	276.5	22.3	228	4	AAAG63856	Amino aci								
143	276.5	22.3	238	2	AAE13208	Staphyloc								
144	276.5	22.3	239	2	AA906258	Staphyloc								
145	276.5	22.3	239	2	AA906257	Staphyloc								
146	276.5	22.3	240	6	ABG71373	Staphyloc								
147	276.5	22.3	240	6	ABG71374	Staphyloc								
148	276	22.3	265	3	AA970105	Mutant St								
149	267.5	21.6	239	2	AAE13207	Staphyloc								
150	267.5	21.6	239	2	AAE45015	Staphyloc								
151	267.5	21.6	239	5	ABB76238	Staphyloc								
152	267.5	21.6	260	8	ADF89842	Streptoco								
153	266.5	21.5	266	7	ABU79070	S. aureus								
154	266.5	21.5	266	7	ADF43292	Staphyloc								
155	265.5	21.4	239	2	AA906251	Staphyloc								
156	265.5	21.4	239	4	AAAB67342	Staphyloc								
157	265.5	21.4	240	6	ABG71367	Staphyloc								
158	258.5	20.9	266	3	AA970108	Staphyloc								
159	258.5	20.9	266	5	ABB79507	Staphyloc								
160	258.5	20.9	266	6	ABU10087	Streptoco								
161	258.5	20.9	266	7	ABU62330	S. aureus								
162	258.5	20.9	266	7	AAE37682	Staphyloc								
163	256.5	20.7	220	7	ABU62334	Streptoco								
164	256.5	20.7	220	7	AAE37687	Streptoco								
165	256.5	20.7	468	7	ABU62335	SPEA L42R								
166	256.5	20.7	468	7	AAE37684	Streptoco								
167	256	20.7	209	8	ADG69997	Streptoco								
168	256	20.7	233	3	AA93741	Amino aci								
169	254.5	20.6	220	7	AAE37689	S. pyogen								
170	253.5	20.5	220	7	AAE37688	S. pyogen								
171	253.5	20.5	468	7	AAE37691	S. pyogen								

ALIGNMENTS

RESULT 1

ABP58456
ID ABP58456 standard; protein; 233 AA.

XX AC ABP58456;

XX DT 14-APR-2003 (first entry)

XX DE Staphylococcal enterotoxin E.

XX KW Superantigen; staphylococcal enterotoxin E; antibody; cancer; tumour;
cytostatic; vaccine.

XX OS Staphylococcus sp.

XX FN WO2003002143-A1.

XX PD 09-JAN-2003.

XX PF 19-JUN-2002; 2002WO-SE001188.

XX PR 28-JUN-2001; 2001SE-00002327.

XX PA (ACTI-) ACTIVE BIOTECH AB.

XX PI Forsberg G, Erlandsson E, Antonsson P, Walse B;

XX DR WPI; 2003-201467/19.

XX PT Conjugate for therapy, has bacterial superantigen with a region in T-cell
receptor and four regions to determine binding to class II major
PT histocompatibility complex, antibody to cancer associated cell surface
structure.

XX PS Example 3; Fig 4; 102pp; English.

XX CC The present sequence is the protein sequence of staphylococcal
enterotoxin SEB. The invention provides novel conjugates (see ABP58454)
CC for human cancer therapy. These comprise an engineered bacterial

CC superantigen, such as novel SEA/E-120 (see ABP58455), which is based on
CC SEE, and an antibody moiety, such as tumour reactive antibody 574. The
CC superantigen is engineered to reduce seroreactivity whilst maintaining
CC biological activity and production levels. The conjugates are designed to
CC target and destroy cancer cells, including cancer of the lung, breast
CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
XX
SQ Sequence 233 AA;

Query Match 100.0%; Score 1238; DB 6; Length 233;
Best Local Similarity 100.0%; Pred. No. 7e-116;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSEIQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSEIQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60

QY 61 HPWYNDLLVLDLGSKDATNKYKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
DB 61 HPWYNDLLVLDLGSKDATNKYKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120

QY 121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180

QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHLIDLYLYTT 233
DB 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHLIDLYLYTT 233

RESULT 2
AAU14103
ID AAU14103 standard; peptide; 257 AA.
XX AAU14103;
AC AAU14103;
XX
DT 21-NOV-2001 (first entry)
XX
DE Peptide sequence from Staphylococcus aureus enterotoxin type E.
XX
KW Anti-retroviral; DP178-like; DP107-like; enterotoxin type E;
KW antifusogenic; antiviral; HIV transmission.
XX
OS Staphylococcus aureus.
XX
XX WO200151673-A2.
XX
XX 19-JUL-2001.
XX
XX 05-JUL-2000; 2000WO-US035727.
XX
XX 09-JUL-1999; 99US-00350841.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
XX WPI; 2001-442157/47.
XX
XX Identifying a compound that inhibits the formation of or disrupts a
PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
PT or intracellular modulatory activity, by detecting the formation of a
PT DP107/DP178 complex.
XX
PS Disclosure; Fig 41; 259pp; English.
XX
XX The present invention relates to peptides which exhibit anti-retroviral
CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
CC amino acids 639-673 of the transmembrane protein gp41 from human
CC immunodeficiency virus 1 (HIV-1) isolate IAI. The DP107 peptide
CC corresponds to amino acids 558-595 of gp41 from HIV-1IAI. The invention
CC also relates to a method of identifying compounds that inhibit the

CC formation of or disrupts a DP107/DP178 complex. The method comprises
CC detecting the formation of a DP107/DP178 complex, both in the presence or
CC absence of a test compound, in a reaction mixture containing DP107 and
CC DP178 peptides. The method is useful for identifying compounds, including
CC small molecule compounds, which may themselves exhibit antifusogenic,
CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
CC peptides are useful to inhibit human and non-human retroviral,
CC particularly HIV, transmission to uninfected cells. The present sequence
CC E represents a peptide sequence from Staphylococcus aureus enterotoxin type
XX
SQ Sequence 257 AA;

Query Match 100.0%; Score 1238; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 8.1e-116;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSEIQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSEIQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 61 HPWYNDLLVLDLGSKDATNKYKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVLDLGSKDATNKYKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 144

QY 121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHLIDLYLYTT 233
DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHLIDLYLYTT 257

RESULT 3
ABO10268
ID ABO10268 standard; protein; 257 AA.
XX
AC ABO10268;
XX
DT 19-AUG-2003 (first entry)
XX
DE S. aureus enterotoxin E.
XX
KW HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
KW Epstein-Barr virus infection; heptad repeat motif.
XX
OS Staphylococcus aureus.
XX
XX US6518013-B1.
XX
XX 11-FEB-2003.
XX
XX 07-JUN-1995; 95US-00485546.
XX
XX 07-JUN-1993; 93US-00073028.
XX
XX 07-JUN-1994; 94US-00255208.
XX
XX 20-DEC-1994; 94US-00360107.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Barney SO, Lambert DM, Petteway SR;
XX WPI; 2003-465599/44.
XX
XX Inhibiting transmission of Epstein-Barr virus to a cell, by contacting
PT the cell with a peptide consisting of a region of Epstein-Barr virus
PT protein.
XX
XX Example; Fig 41; 716pp; English.
XX
XX The invention relates to inhibiting (M) transmission of an Epstein-Barr
CC virus to a cell, comprising contacting the cell with an effective

concentration of a peptide consisting of a region of 16-39 consecutive amino acids of an Epstein-Barr virus protein for an effective period of time, where the region is recognised by one or more of ALLMOTIS, 107x178x4 or PL21P sequence search motifs, the peptide further comprises an amino terminal X, and a carboxy terminal Z in which X comprises an amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic group or macromolecular carrier group, and Z comprises a carboxyl group, amido group, hydrophobic group, or macromolecular carrier group, and fusion of the virus to the cell is inhibited. The peptides were identified by analysing the structure/motifs present in the HIV-1 glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat motif containing peptides were used to design the motifs cited above, which in turn were used to analyse proteins from other pathogenic organisms and HIV isolates, looking for DP107/178 structural analogues. The method is useful for inhibiting transmission of Epstein-Barr virus to a cell and Epstein-Barr virus infection. The present sequence is a protein from a pathogenic organism analysed for regions analogous to DP107 or DP178

XX Sequence 257 AA;

Query Match 100.0%; Score 1238; DB 6; Length 257;
Best Local Similarity 100.0%; Pred. No. 8.1e-116;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEENEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFTG 60
Dd 25 SEKSEENEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFTG 84
Qy 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTENKTKACMYGGVTLHDNNRLT 120
Dd 85 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTENKTKACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHLYHGKFGLYNSDSFGGKVQ 180
Dd 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHLYHGKFGLYNSDSFGGKVQ 204
Qy 181 RGLVVFHSSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENLHIDLILYTT 233
Dd 205 RGLVVFHSSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENLHIDLILYTT 257

RESULT 4
ADF89830
ID ADF89830 standard; protein; 257 AA.

AC ADF89830;

XX 26-FEB-2004 (first entry)

XX Staphylococcal enterotoxin E (SEE) superantigen.

XX Superantigen; SAg; Staphylococcal enterotoxin; SE; SEE; cytostatic;
KW gene therapy; cancer.

XX Staphylococcus sp.

OS WO2003094846-A2.

XX 20-NOV-2003.

XX 08-MAY-2003; 2003WO-US014381.

XX 08-MAY-2002; 2002US-0378988P.

XX 15-JUN-2002; 2002US-0389366P.

XX 28-AUG-2002; 2002US-0406697P.

XX 29-AUG-2002; 2002US-0406750P.

XX 01-OCT-2002; 2002US-0415310P.

XX 02-OCT-2002; 2002US-0415400P.

XX 09-JAN-2003; 2003US-0438686P.

XX (TERM/) TERMAN D S.

PI Terman DS;
XX WPI; 2004-011997/01.
XX Treating a subject with cancer or malignant diseases comprises
PT intratumoral, intrathecal or intracavitary administration of an amount of
PT a superantigen composition to the subject.
XX
PS Disclosure; SEQ ID NO 7; 91pp; English.

XX The invention relates to treating a subject with cancer. The method
CC involves administering an amount of a superantigen (SAG) composition
CC comprising a molecule selected from: a native SAG protein; its
CC biologically active fragment or a biologically active homologue or a
CC biologically active fusion protein comprising the SAG or its fragment or
CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
CC exotoxin, Y. pseudotuberculosis SAG, Mycoplasma arthritides SAG and
CC Clostridium perfringens exotoxin. The method is useful in treating cancer
CC or malignant diseases such as malignant pleural effusion, ascites,
CC pericardial effusion or meningeal carcinomatosis. The present sequence
CC represents a Staphylococcal enterotoxin E (SEE) superantigen.

XX Sequence 257 AA;

Query Match 100.0%; Score 1238; DB 8; Length 257;
Best Local Similarity 100.0%; Pred. No. 8.1e-116;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEENEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFTG 60
Dd 25 SEKSEENEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFTG 84
Qy 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTENKTKACMYGGVTLHDNNRLT 120
Dd 85 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTENKTKACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHLYHGKFGLYNSDSFGGKVQ 180
Dd 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHLYHGKFGLYNSDSFGGKVQ 204
Qy 181 RGLVVFHSSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENLHIDLILYTT 233
Dd 205 RGLVVFHSSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENLHIDLILYTT 257

RESULT 5

AAB67339

ID AAB67339 standard; peptide; 230 AA.

XX AAB67339;

XX 23-APR-2001 (first entry)

XX Staphylococcus aureus enterotoxin E protein.

XX Tumour; cancer; immune; enterotoxin.

XX Staphylococcus aureus.

XX US6180097-B1.

XX 30-JAN-2001.

XX 30-OCT-1998; 98US-00183437.

XX 03-OCT-1989; 89US-00416530.

XX 17-JAN-1990; 90US-00466577.

XX 17-JAN-1991; 91WO-US000342.

XX 01-JUN-1992; 92US-00891718.

XX 02-MAR-1993; 93US-00025144.

XX 31-JAN-1994; 94US-00189424.

XX 19-JUN-1995; 95US-00491746.

XX (TERM/) Terman D S.
 PA Terman DS;
 XX WPI; 2001-158657/16.
 XX Tumor cell capable of stimulating antitumor immune reactivity in vitro or
 PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
 PT costimulatory molecule.
 XX Disclosure; Fig 2; 16pp; English.
 XX The present invention relates to a tumour cell capable of stimulating
 CC antitumor immune reactivity in vitro or in vivo contains and expresses an
 CC exogenous nucleic acid molecule encoding a superantigen or its active
 CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
 CC molecule that activates T cells in conjunction with an antigenic
 CC stimulus. The invention may be used for cancer therapy by stimulating an
 CC anticancer immune response in vivo or ex vivo
 XX Sequence 230 AA;
 PS Query Match 98.9%; Score 1224; DB 4; Length 230;
 XX Best Local Similarity 100.0%; Pred. No. 1.8e-114; Indels 0; Gaps 0;
 XX Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 SEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 63
 DB 1 SEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 60
 QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYYGQCAGGTPNKTCMYGGVTLHDNNRLTEEK 123
 DB 61 YNDLLVDLGSKDATNKYKGGKVDLYGAYYGQCAGGTPNKTCMYGGVTLHDNNRLTEEK 120
 QY 124 KVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQGL 183
 DB 121 KVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQGL 180
 QY 184 IVFHSSEGSTSVSYDLFDAQQYPTDLLRIYRDNKTINSENHLIDLTYLT 233
 DB 181 IVFHSSEGSTSVSYDLFDAQQYPTDLLRIYRDNKTINSENHLIDLTYLT 230
 RESULT 6
 AAW35374 standard; peptide; 245 AA.
 XX AAW35374;
 XX 20-APR-1998 (first entry)
 XX Staphylococcus enterotoxin in SEE wild-type superantigen.
 XX SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
 KW cancer; infection; autoimmune disease; antibody.
 XX Staphylococcus sp.
 XX Key Location/Qualifiers
 FH Misc-difference 20 /note= "can be mutated at this position"
 FT Misc-difference 21 /note= "can be mutated at this position"
 FT Misc-difference 24 /note= "can be mutated at this position"
 FT Misc-difference 27 /note= "can be mutated at this position"
 FT Misc-difference 27 /note= "can be mutated at this position"
 XX WO9736932-A1.
 XX 09-OCT-1997.
 XX

PF 26-MAR-1997; 97WO-SE000537.
 XX 29-MAR-1996; 96SE-00001245.
 PR 12-AUG-1996; 96US-00695692.
 XX (PHAA) PHARMACIA & UPJOHN AB.
 XX Antonsson P, Hansson J, Bjoerk P, Dohlsten M, Kalland T;
 PI Abrahmeen L, Forsberg G;
 XX WPI; 1997-503052/46.
 XX Conjugate of target seeking moiety and modified superantigen - useful for
 PT activating the immune system to treat cancer, viral infections, parasitic
 PT infections and autoimmune diseases.
 XX Claim 4; Page 38-39; 58pp; English.
 XX This is the wild-type Staphylococcus enterotoxin SEE superantigen. This
 CC SEE superantigen can be modified to be used in a novel conjugate. The
 CC novel conjugate comprises a target seeking moiety and a modified wild
 CC type superantigen. The modified superantigen retains its ability to
 CC activate a subset of T cells, even though 1 or more wild-type amino acid
 CC residues in at least 1 region which functions in determining binding to T
 CC cell receptor (TCR) and activation of a subset of T cells has/have been
 CC replaced. Such a modified superantigen can optionally be used as part of
 CC a conjugate with a target seeking moiety, for activating the immune
 CC system to treat a mammalian disease. A pharmaceutical composition can be
 CC prepared comprising a modified antibody (preferably a Fab fragment fused
 CC to a peptide moiety providing activation of T cells in Vbeta specific
 CC manner) in which cysteines providing for interchain cysteine linkages in
 CC the native antibody have been replaced (preferably by serine residues) to
 CC prohibit cysteine formation. The modified wild-type superantigen is used
 CC for treating cancer, viral infections, parasitic infestations and
 CC autoimmune disease. The modified wild type superantigen has a lower
 CC immunogenicity and reactivity with neutralising antibodies and has fewer
 CC side-effects when used as a drug, compared to wild type superantigen
 XX Sequence 245 AA;
 PS Query Match 98.7%; Score 1222; DB 2; Length 245;
 XX Best Local Similarity 95.1%; Pred. No. 3.1e-114; Indels 12; Gaps 1;
 XX Matches 233; Conservative 0; Mismatches 0; Indels 12; Gaps 1;
 QY 1 SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 1 SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGQCAGGTPNKTCMYGGVTLHDNNRLT 120
 DB 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGQCAGGTPNKTCMYGGVTLHDNNRLT 120
 QY 121 ERKKYPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 121 ERKKYPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 QY 181 RGLIVFHSSEGSTSVSYDLFDAQQYPTDLLRIYRDNKTINSENHLIDLTYLTINSENHLIDL 228
 DB 181 RGLIVFHSSEGSTSVSYDLFDAQQYPTDLLRIYRDNKTINSENHLIDLTYLTINSENHLIDL 240
 QY 229 YLYTT 233
 DB 241 YLYTT 245
 RESULT 7
 ABP58457 standard; protein; 233 AA.
 ID ABP58457
 XX AC ABP58457;
 XX DT 14-APR-2003 (first entry)
 XX


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QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGPFPTG 60
DB 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGPFPTG 60
QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSEGSTSVSYDLFDAQGGYPTDLLRIYRDNK-----TINSENLHIDL 228
DB 181 RGLIVFHSSEGSTSVSYDLFDAQGGYPTDLLRIYRDNKINSENLHIDL 240
QY 229 YLYTT 233
DB 241 YLYTT 245

RESULT 9
ABU79072
ID ABU79072 standard; protein; 248 AA.
AC ABU79072;
XX
DT 18-JUN-2003 (first entry)
DE S. aureus SEE (staphylococcus enterotoxin E) protein.
KW Superantigen; SAG; staphylococcal enterotoxin; tumour; cancer; apoptosis;
KW Gene therapy; mammalian cell receptor; tumour associated lipid; anergy;
KW T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
KW APC; antitumour.
XX
OS Staphylococcus aureus.
XX
PN US2002177551-A1.
XX
PD 28-NOV-2002.
XX
PF 30-MAY-2001; 2001US-00870759.
XX
PR 31-MAY-2000; 2000US-0208128P.
XX
PA (TERM/) TERMAN D S.
XX
PI Terman DS;
XX
WPI; 2003-361759/34.
DR N-PSDB; ACA64698.
XX
XX
PT A mammalian cell receptor, useful in the treatment of cancer by binding
PT to tumor associated lipids where the binding induces anergy or apoptosis
PT in T cells and antigen presenting cells.
XX
PS Disclosure; Page; 167pp; English.
XX
XX The invention relates to a mammalian cell receptor, useful in the
XX treatment of cancer, which binds to tumour associated lipids and induces
XX anergy or apoptosis in the T cells and antigen presenting cells (APCs).
XX Also included are a mammalian cell useful in the treatment of cancer
XX where the receptor which binds tumour associated lipids and induces
XX cellular inactivation or death is deleted or functionally deactivated,
XX producing (M1) a tumouricidal immunocyte population in vivo in a mammal
XX (by allowing tumour associated lipids to contact immunocytes in which
XX receptors for immunosuppressive fatty acids, ceramides, glycolipids,
XX sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
XX sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
XX deleted), a construct useful in the treatment of cancer comprising a
XX superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
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CC useful in the treatment of cancer (where an adaptor protein which
CC inhibits T cell activation by tumour associated antigens is deleted or
CC functionally deactivated), a composition useful in the treatment of
CC cancer (comprising a lipid raft conjugated to a superantigen), producing
CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
CC allowing tumour associated lipids to contact immunocytes, in which
CC receptors for the lipids are inactivated or deleted to produce a
CC tumouricidal immunocyte population, and administering the tumouricidal APC
CC activated immunocytes to the host), producing (M3) a tumouricidal APC
CC population ex vivo in a mammal (by allowing a tumour associated lipid to
CC contact APCs, in which receptors for the tumour associated lipids are
CC inactivated or deleted to produce a tumouricidal activated population,
CC and administering APCs to the host), producing a tumouricidal T cell
CC population ex vivo in a mammal) by allowing a tumour associated lipids to
CC contact T cells, in which adaptor proteins, which inhibit T cell
CC activation by tumour associated antigens, are deleted or functionally
CC deactivated to produce a tumouricidal population of T cells, and
CC administering the tumouricidal activated T cells to the host, or
CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
CC administering the tumouricidal activated T cells to the host), treating
CC (M5) cancer in a mammal (by administering a lipid binding molecule which
CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
CC a tumouricidal T cell population in vivo in a mammal (by allowing a
CC tumour associated antigen to contact immunocytes in which adaptor
CC proteins which inhibit T cell activation by tumour associated antigens
CC are deleted or functionally deactivated) and producing (M7) a
CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
CC receptors, methods and compositions are useful for treating cancers and
CC tumours. Bacterial superantigens are co-administered or administered as
CC fusion constructs with anti-tumour proteins or motifs. The present
CC sequence represents a bacterial superantigen protein (e.g. a
CC staphylococcal enterotoxin). Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format from the US patent office website at
CC "seqdata.uspto.gov/sequence.html?docID=20020177551"
XX
SQ Sequence 248 AA;

Query Match 96.0%; Score 1188; DB 6; Length 248;
Best Local Similarity 100.0%; Pred. No. 8.2e-111;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGPFPTG 60
DB 25 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGPFPTG 84
QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQGGYPTDLLRIYRDNKINSENL 224
DB 205 RGLIVFHSSEGSTSVSYDLFDAQGGYPTDLLRIYRDNKINSENL 248

RESULT 10
ADF43296
ID ADF43296 standard; protein; 248 AA.
XX
AC ADF43296;
XX
DT 12-FEB-2004 (first entry)
XX
DE Staphylococcal enterotoxin E polypeptide seq id 16.
XX
XX receptor, lipid-based tumour associated antigen; cytostatic;
KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
KW infectious disease; Staphylococcal enterotoxin E; SEE; enterotoxin E.
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XX Staphylococcus.
OS
XX
PN US2003157113-A1.
XX
XX 21-AUG-2003.
PD
XX
PF 28-DEC-2000; 2000US-00751708.
XX
XX 28-DEC-1999; 99US-0173371P.
PR
XX
XX (TERM/) TERMAN D S.
PA
XX
XX Terman DS;
PI
XX
XX WPI; 2003-787326/74.
DR
XX
XX New receptor in a mammalian cell that inhibits regular activation by
PT receptors specific for lipid-based tumor associated antigens, useful for
PT treating a neoplastic disease or tumor, and infectious diseases.
XX
XX Example 3; SEQ ID NO 16; 151pp; English.
PS
XX
XX The invention describes a receptor in a mammalian cell that inhibits
CC regular activation by receptors specific for lipid-based tumour
CC associated antigen. The receptor has cytostatic and antimicrobial
CC properties and is suitable for use in gene therapy. The receptors,
CC methods and compositions are useful for treating a neoplastic disease or
CC tumour (cancer), and infectious diseases. This is the amino acid sequence
CC of an enterotoxin superantigen polypeptide the DNA encoding which can be
CC transfected in to a cell alone or with DNA encoding a cell surface moiety
CC to generate antitumour immunity.
XX
XX Sequence 248 AA;
SQ
Query Match 96.0%; Score 1188; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 8.2e-111;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEKEINEKDLRKSEIQNALSNLRQIYYNEKAITENKESDDQFLENTLLKGFPTG 60
DB 25 SEKEINEKDLRKSEIQNALSNLRQIYYNEKAITENKESDDQFLENTLLKGFPTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYQPTDLLRIYRDNKTINSEN 224
DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYQPTDLLRIYRDNKTINSEN 248
RESULT 11
AAR45012
ID AAR45012 standard; protein; 230 AA.
XX
XX AAR45012;
AC
XX
XX 25-MAR-2003 (revised)
DT
XX
XX 08-JUN-1994 (first entry)
DT
XX
XX Staphylococcal enterotoxin SEE.
DE
XX
XX Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KW autoimmune disease; toxicity; Protein A; perfusion system.
XX
XX Staphylococcus aureus.
OS
XX
XX Key Location/Qualifiers
FH

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FT Misc-difference 120
FT /note= "Given in the specification as J, no further
FT details given"
FT Misc-difference 121
FT /note= "Given in the specification as J, no further
FT details given"
FT Misc-difference 123
FT /note= "Given in the specification as O, no further
FT details given"
FT Misc-difference 124
FT /note= "Given in the specification as U, no further
FT details given"
XX
XX WO9324136-A1.
PN
XX
XX 09-DEC-1993.
PD
XX
XX 01-JUN-1993; 93WO-US005213.
PF
XX
XX 01-JUN-1992; 92US-00891718.
PR
XX
XX (TERM/) TERMAN D S.
PA
XX (STON/) STONE J L.
PA
XX Terman DS, Stone JL;
XX
XX WPI; 1993-405418/50.
XX
XX Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
PT in a patient or for the treatment of auto-immune diseases.
XX
XX Disclosure; Fig 1; 90pp; English.
XX
XX The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer in
CC a patient. These SEs, and homologues of them, can be used as tumouricidal
CC agents for treating cancers and autoimmune disease. They exhibit
CC tumouricidal activity and toxicity identical to that observed for the
CC Protein A perfusion system. They may be administered by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 230 AA;
SQ
Query Match 95.2%; Score 1179; DB 2; Length 230;
Best Local Similarity 96.1%; Pred. No. 6e-110;
Matches 221; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 4 SEINEKDLRKSEIQNALSNLRQIYYNEKAITENKESDDQFLENTLLKGFPTGHPW 63
DB 1 SEINEKDLRKSEIQNALSNLRQIYYNEKAITENKESDDQFLENTLLKGFPTGHPW 60
QY 64 YNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLTEK 123
DB 61 YNDLLVDKSGKDATNKYKGVLDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLTEEX 120
QY 124 KVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 183
DB 121 VXXYBKWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 184 IVFHSSEGSTVSVDLFDAGQGYQPTDLLRIYRDNKTINSENLDLYLYTT 233
DB 181 IVFHSSEGSTVSVDLFDAGQGYQPTDLLRIYRDNKTINSENMDIYLYTT 230
RESULT 12
ABB76235
ID ABB76235 standard; protein; 230 AA.
XX
XX ABB76235;
AC
XX
XX 09-AUG-2002 (first entry)
DT
XX
XX Staphylococcus aureus enterotoxin E.
DE

```

XX Enterotoxin E; SEE, superantigen; antigen; tumour; cancer; antitumour;
 KW therapy.
 XX Staphylococcus aureus.
 XX Key Location/Qualifiers
 FH Misc-difference 120 /note= "given as 'J' in the specification"
 FT Misc-difference 121 /note= "given as 'J' in the specification"
 FT Misc-difference 123 /note= "given as 'O' in the specification"
 FT Misc-difference 124 /note= "given as 'U' in the specification"
 FT Misc-difference 125 /note= "given as 'V' in the specification"
 XX US2002051765-A1.
 PN XX
 PD XX
 XX 02-MAY-2002.
 XX 19-DEC-2000; 2000US-00741503.
 XX 03-OCT-1989; 89US-00416530.
 PR 17-JAN-1990; 90US-00466577.
 PR 17-JAN-1991; 91WO-US000342.
 PR 01-JUN-1992; 92US-00891718.
 PR 02-MAR-1993; 93US-00025144.
 PR 31-JAN-1994; 94US-00189424.
 PR 19-JUN-1995; 95US-00491746.
 XX (TERM/) Terman D S.
 PA Terman DS;
 XX WPI; 2002-415198/44.
 XX Reagent for treating cancer without the need for e.g. radiotherapy,
 PT comprises a specific V beta subset of T cells sensitized to a growing
 PT tumor and stimulated with superantigens.
 XX Disclosure; Fig 2; 17pp; English.
 XX The present sequence is the protein sequence of enterotoxin E (SEE) of
 CC Staphylococcus aureus. Similarity is shown, in several stretches of
 CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
 CC exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the
 CC present invention, synthetic polypeptides useful in tumour therapy and in
 CC blocking or destroying autoreactive T and B lymphocyte populations are
 CC characterised by substantial structural homology to staphylococcal
 CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
 CC exotoxins, with statistically significant sequence homology and
 CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
 CC analysis exceeding 6) to include alignment of cysteine residues and
 CC similar hydrophathy profiles. These superantigens are used to treat solid
 CC tumours, including their metastases, without radiation, surgery or
 CC standard chemotherapeutic agents. A claimed method of human cancer
 CC treatment involves contacting haematopoietic cells from a patient with
 CC one or more superantigens ex vivo to generate stimulated cells, selecting
 CC a specific V beta subset of cells, and reintroducing these cells into the
 CC patient to induce an in vivo therapeutic, tumouricidal reaction
 XX Sequence 230 AA;
 SQ
 Query Match 94.9%; Score 1175; DB 5; Length 230;
 Best Local Similarity 96.1%; Pred. No. 1.5e-109;
 Matches 221; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 QY 4 SEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 63
 DB 1 SEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 60

QY 64 YNDLLVLDGSKDANTNKGKVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLTEEK 123
 DB 61 YNDLLVLDGSKDANTNKGKVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLTEEX 120
 QY 124 KVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQVRL 183
 DB 121 XVXXKXWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQVRL 180
 QY 184 IVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHLIDLYLYTT 233
 DB 181 IVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHDIYLYTT 230
 RESULT 13
 AAR13204
 ID AAR13204 standard; protein; 230 AA.
 XX AAR13204;
 AC AAR13204;
 XX 15-OCT-1991 (first entry)
 DT XX
 DE Staphylococcal enterotoxin E.
 XX SEE; cancer treatment; pyrogen; tumouricide.
 KW Staphylococcus aureus.
 XX WO9110680-A.
 OS 25-JUL-1991.
 PN 17-JAN-1990; 90US-00466577.
 PD 17-JAN-1990; 90US-00466577.
 PF (TERM/) Terman D S.
 PR Terman DS;
 XX WPI; 1991-237984/32.
 XX Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity as
 PT Staphylococcal protein A without potential toxic reactions.
 XX Disclosure; Fig 1; 74pp; English.
 XX SEE was isolated and purified from S.aureus. It can be used for treating
 CC cancer, activating cytokine mediators and procoagulant systems,
 CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
 CC administered intravenously, optionally with ibuprofen to attenuate toxic
 CC reaction to SEE. Synthetic polypeptides having structural homology to
 CC Staphylococcal exotoxins are claimed, provided the homology includes
 CC statistically significant sequence homology, alignment of Cysteine
 CC residues and similar hydrophathy profiles. See AAR13203-R13211
 XX Sequence 230 AA;
 SQ
 Query Match 93.4%; Score 1156; DB 2; Length 230;
 Best Local Similarity 93.9%; Pred. No. 1.2e-107;
 Matches 216; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 QY 4 SEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 63
 DB 1 SEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 60
 QY 64 YNDLLVLDGSKDANTNKGKVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLTEEK 123
 DB 61 YNDLLVLDGSKDANTNKGKVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLTEEX 120
 QY 124 KVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQVRL 183
 DB 121 XVXXKXWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQVRL 180

QY 184 IVFHSSEGSTVSYDLFDAQGOVPTLLRIYRDNKTINSENHLIDLYLTT 233
|||||
Db 181 IVFHSSEGSTVSYDLFDAQGOVPTLLRIYRDNKTINSENHLIDLYLTT 230
|||||
RESULT 14
ABP58455
ID ABP58455 standard; protein; 233 AA.
XX
AC ABP58455;
XX
XX 14-APR-2003 (first entry)
XX
XX Engineered superantigen SEA/E-120 for human cancer therapy.
XX
XX Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;
KW cytosstatic; vaccine; SEA/E-120; mutant; mutein.
XX
XX Staphylococcus sp.
OS Synthetic.
OS
FH Key Location/Qualifiers
FT Misc-difference 20 /note= "wild-type Arg substituted by Gly"
FT Misc-difference 21 /note= "wild-type Asn substituted by Thr"
FT Misc-difference 24 /note= "wild-type Ser substituted by Gly"
FT Misc-difference 27 /note= "wild-type Arg substituted by Lys"
FT Misc-difference 79 /note= "wild-type Lys substituted by Glu"
FT Misc-difference 81 /note= "wild-type Lys substituted by Glu"
FT Misc-difference 83 /note= "wild-type Lys substituted by Ser"
FT Misc-difference 84 /note= "wild-type Lys substituted by Ser"
FT Misc-difference 227 /note= "wild-type Asp substituted by Ser"
XX
XX WO2003002143-A1.
XX
XX 09-JAN-2003.
XX
XX 19-JUN-2002; 2002WO-SE001188.
XX
XX 28-JUN-2001; 2001SE-00002327.
XX
XX (ACTI-) ACTIVE BIOTECH AB.
XX
XX Forsberg G, Erlandsson E, Antonsson P, Walse B;
FI WPI; 2003-201467/19.
XX
XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
PT receptor and four regions to determine binding to class II major
PT histocompatibility complex, antibody to cancer associated cell surface
PT structure.
XX
XX Claim 8; Fig 2; 102pp; English.
XX
XX The present sequence is the protein sequence of engineered staphylococcal
CC superantigen SEA/E-120. The superantigen is derived from staphylococcal
CC enterotoxin E (SEE) by the incorporation of the following amino acid
CC substitutions to reduce seroreactivity whilst maintaining production
CC levels and biological activity: R20G, N21T, S24G, R27K, K79E, K81E, K83S
CC and D227S. SEA/E-120 has been genetically fused to the Fab moiety of the
CC tumour reactive antibody S14 to form a claimed conjugate (see ABP58454)
CC designed to target and destroy cancer cells, including cancer of the
CC lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and
CC prostate (claimed)

XX Sequence 233 AA;
SQ
Query Match 89.4%; Score 1107; DB 6; Length 233;
Best Local Similarity 89.7%; Pred. No. 1.1e-102;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 1 SEKSEEINEKDLRKKSLORNALSNLRQIYYVYNEKAITENKESDDQPLENTLLFKGFTTG 60
|||||
Db 1 SEKSEEINEKDLRKKSSELOGTALGNLQIYYVYNSKAITSEKKSADQFLTNTLLFKGFTTG 60
|||||
QY 61 HPWYNLLVDLGSKDATNKYKGVKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
|||||
Db 61 HPWYNLLVDLGSKTAATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
|||||
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
|||||
Db 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
|||||
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOVPTLLRIYRDNKTINSENHLIDLYLTT 233
|||||
Db 181 RGLIVFHSSEGSTVSYDLFDAQGOVPTLLRIYRDNKTINSENHLIDLYLTT 233
|||||
RESULT 15
ABP58454
ID ABP58454 standard; protein; 672 AA.
XX
XX AC ABP58454;
XX
XX 14-APR-2003 (first entry)
XX
XX Engineered superantigen for human cancer therapy.
XX
XX Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;
KW cytosstatic; vaccine; human; SEA/E-120; mutant; mutein.
XX
XX Homo sapiens.
OS Staphylococcus sp.
OS Synthetic.
OS Chimeric.
XX
XX Key Location/Qualifiers
FH Region 1..120
FT /note= "S14 variable heavy chain"
FT Misc-difference 41 /note= "wild-type His substituted by Pro"
FT Misc-difference 44 /note= "wild-type Ser substituted by Gly"
FT Misc-difference 69 /note= "wild-type Ile substituted by Thr"
FT Misc-difference 113 /note= "wild-type Val substituted by Gly"
FT Region 121..222
FT /note= "C242 constant heavy chain"
FT Region 226..458
FT /note= "SEA/E-120"
FT Misc-difference 245 /note= "wild-type Arg substituted by Gly"
FT Misc-difference 246 /note= "wild-type Asn substituted by Thr"
FT Misc-difference 249 /note= "wild-type Ser substituted by Gly"
FT Misc-difference 252 /note= "wild-type Arg substituted by Lys"
FT Misc-difference 304 /note= "wild-type Lys substituted by Glu"
FT Misc-difference 306 /note= "wild-type Lys substituted by Glu"
FT Misc-difference 308 /note= "wild-type Lys substituted by Ser"
FT Misc-difference 309 /note= "wild-type Lys substituted by Ser"
FT

FT Misc-difference 452 /note= "wild-type Asp substituted by Ser"
FT Region 459. .565
FT /note= "S74 variable light chain"
FT Misc-difference 469 /note= "wild-type Phe substituted by Ser"
FT Misc-difference 504 /note= "wild-type Thr substituted by Lys"
FT Misc-difference 522 /note= "wild-type Ile substituted by Ser"
FT Misc-difference 532 /note= "wild-type Phe substituted by Leu"
FT Misc-difference 536 /note= "wild-type Thr substituted by Ser"
FT Misc-difference 537 /note= "wild-type Leu substituted by Val"
FT Misc-difference 542 /note= "wild-type Leu substituted by Ala"
FT Region 566. .672
FT /note= "C242 constant light chain"
XX WO2003002143-A1.
PN
XX
XX
PD 09-JAN-2003.
XX
PF 19-JUN-2002; 2002WO-SE001188.
XX
PR 28-JUN-2001; 2001SE-00002327.
XX
PA (ACTI-) ACTIVE BIOTECH AB.
XX
PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
PI WPI; 2003-201467/19.
DR
XX
XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
PT receptor and four regions to determine binding to class II major
PT histocompatibility complex, antibody to cancer associated cell surface
PT structure.
XX
PS Claim 12; Fig 10; 102pp; English.
XX
CC The present sequence is a conjugate of a bacterial superantigen and an
CC antibody moiety, and has been designed to target and destroy cancer
CC cells. The bacterial superantigen is SEA/E-120 (see also ABP8455), which
CC was derived from staphylococcal enterotoxin E (SEE) by the incorporation
CC of the following amino acid substitutions to reduce seroreactivity whilst
CC maintaining production levels and biological activity: R20G, N21T, S24G,
CC R27K, K79E, K81E, K83S and D227S. SEA/E-120 was genetically fused to the
CC Fab moiety of the tumour reactive antibody 574. Substitutions were made
CC in the 574 sequence to obtain higher yields: in the heavy chain, H41P,
CC S44G, I69T and V113G; and in the light chain, F10S, T45K, I63S, F73L,
CC T77S, L78V and L83A. An expression vector comprising DNA encoding the
CC conjugate can be used to transform host cells for recombinant production
CC of the conjugate. The conjugate is useful for treating cancer, including
CC cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach,
CC cervix and prostate (claimed)
XX
SQ Sequence 672 AA;

Query Match 89.4%; Score 1107; DB 6; Length 672;
Best Local Similarity 89.7%; Pred. No. 4.9e-102;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 226 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 285

QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACWGGVTLHDNNRLT 120
DB 286 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACWGGVTLHDNNRLT 345

QY 121 EKKKVPINLWIDGKQTTVPIDKVKTSKEVTQVELDLQARHYLHGKFGLYNSDSFGCKVQ 180

DB 346 EKKKVPINLWIDGKQTTVPIDKVKTSKEVTQVELDLQARHYLHGKFGLYNSDSFGCKVQ 405
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRLRIYRDNKTINSENHLIDLYLTT 233
DB 406 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRLRIYRDNKTINSENHLIDLYLTT 458

RESULT 16
AAR13203
ID AAR13203 standard; protein; 233 AA.
XX
AC AAR13203;
XX 15-OCT-1991 (first entry)
XX Staphylococcal enterotoxin A.
DE
XX
XX SEA; cancer treatment; pyrogen; tumouricide.
XX Staphylococcus aureus.
XX WO9110680-A.
PN
XX
XX 25-JUL-1991.
PD
XX
PF 17-JAN-1990; 9OUS-00466577.
XX
PR 17-JAN-1990; 9OUS-00466577.
XX
PA (TERM/) TERMAN D S.
XX
PI Terman DS;
XX
XX WPI; 1991-237984/32.
DR
XX Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumoricidal activity as
PT Staphylococcal protein A without potential toxic reactions.
XX
XX Disclosure; Fig 1; 74pp; English.
XX
XX SEA was isolated and purified from S.aureus. It can be used for treating
CC cancer, activating cytokine mediators and procoagulant systems,
CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
CC administered intravenously, optionally with ibuprofen to attenuate toxic
CC reaction to SEA. Synthetic polypeptides having structural homology to
CC Staphylococcal exotoxins are claimed, provided the homology includes
CC statistically significant sequence homology, alignment of Cysteine
CC residues and similar hydropathy profiles. See also AAR13204-R13211
XX
SQ Sequence 233 AA;

Query Match 83.6%; Score 1035; DB 2; Length 233;
Best Local Similarity 82.8%; Pred. No. 1.9e-95;
Matches 193; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60

QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACWGGVTLHDNNRLT 120
DB 61 HSWYNLLVDLGSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACWGGVTLHDNNRLT 120

QY 121 EKKKVPINLWIDGKQTTVPIDKVKTSKEVTQVELDLQARHYLHGKFGLYNSDSFGCKVQ 180
DB 121 EKKKVPINLWIDGKQTTVPIDKVKTSKEVTQVELDLQARHYLHGKFGLYNSDSFGCKVQ 180

QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRLRIYRDNKTINSENHLIDLYLTT 233
DB 181 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRLRIYRDNKTINSENHLIDLYLTT 233

RESULT 17
ABP58458
ID ABP58458 standard; protein; 233 AA.
XX AC
XX ABP58458;
XX AC
XX 14-APR-2003 (first entry)
XX DT
XX DE Staphylococcal enterotoxin A.
XX DE Superantigen; staphylococcal enterotoxin A; antibody; cancer; tumour;
XX KW cytostatic; vaccine.
XX KW
XX OS Staphylococcus sp.
XX OS
XX PN WO2003002143-A1.
XX PD
XX PD 09-JAN-2003.
XX PF 19-JUN-2002; 2002WO-SE001188.
XX PF 28-JUN-2001; 2001SE-00002327.
XX PR
XX PA (ACTI-) ACTIVE BIOTECH AB.
XX PA
XX PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
XX PI WPI; 2003-201467/19.
XX DR
XX XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
XX PT receptor and four regions to determine binding to class II major
XX PT histocompatibility complex, antibody to cancer associated cell surface
XX PT structure.
XX PT
XX PS Example 3; Fig 3; 102pp; English.
XX CC The present invention is the protein sequence of staphylococcal
XX CC enterotoxin A (SEA). The invention provides novel conjugates (see
XX CC ABP58454) for human cancer therapy. These comprise an engineered
XX CC bacterial superantigen, such as novel SEA/E-120 (see ABP58455), and an
XX CC antibody moiety, such as tumour reactive antibody 574. Bacterial
XX CC enterotoxins such as SEA, SEE, SED and SEH were used in the molecular
XX CC modelling of the engineered superantigens. The superantigens were
XX CC engineered to reduce seroreactivity whilst maintaining biological
XX CC activity and production levels. The novel conjugates were designed to
XX CC target and destroy cancer cells, including cancer of the lung, breast,
XX CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
XX CC
XX SQ Sequence 233 AA;
Query Match 82.6%; Score 1023; DB 6; Length 233;
Best Local Similarity 82.0%; Pred. No. 3e-94;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
Qy 1 SEKSEINEKDLRKSELRNALSLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
Db 1 SEKSEINEKDLRKSELRQGTALGNLQIYYNEKAKTENKESHDPQLQHTILFKGFTD 60
Qy 61 HPWYNDLLVLDGSDATNKYKGGKVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 120
Db 61 HSWYNDLLVDFDSKDI VDKYKGGKVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 120
Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGGKVQ 180
Db 121 EEKVPINLWIDGKQTTVPLETVTKNKKVTVQELDLQARHYLHGKFLYNSDSFGGKVQ 180
Qy 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNKTINSENHLDIYLTT 233
Db 181 RGLIVFHTSTEPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHLDIYLTS 233

AAU14104
ID AAU14104 standard; peptide; 257 AA.
XX AC
XX AAU14104;
XX DT
XX DT 21-NOV-2001 (first entry)
XX XX
XX DE Peptide sequence from Staphylococcus aureus enterotoxin A.
XX DE Anti-retroviral; DPl78-like; DPl07-like; enterotoxin A; antifusogenic;
XX KW antiviral; HIV transmission.
XX OS Staphylococcus aureus.
XX OS
XX PN WO200151673-A2.
XX XX
XX PD 19-JUL-2001.
XX PF 05-JUL-2000; 2000WO-US035727.
XX PF 09-JUL-1999; 99US-00350841.
XX PR (TRIM-) TRIMERIS INC.
XX PA
XX PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
XX PI WPI; 2001-442157/47.
XX DR
XX XX Identifying a compound that inhibits the formation of or disrupts a
XX PT DPl07/DPl78 complex, especially compounds with antifusogenic, antiviral
XX PT or intracellular modulatory activity, by detecting the formation of a
XX PT DPl07/DPl78 complex.
XX XX
XX PS Disclosure; Fig 42; 259pp; English.
XX CC The present invention relates to peptides which exhibit anti-retroviral
XX CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
XX CC DPl78-like and DPl07-like peptides. The DPl78 peptide corresponds to
XX CC amino acids 639-673 of the transmembrane protein gp41 from human
XX CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DPl07 peptide
XX CC corresponds to amino acids 558-595 of gp41 from HIV-1uAI. The invention
XX CC also relates to a method of identifying compounds that inhibit the
XX CC formation of or disrupts a DPl07/DPl78 complex. The method comprises
XX CC detecting the formation of a DPl07/DPl78 complex, both in the presence or
XX CC absence of a test compound, in a reaction mixture containing DPl07 and
XX CC DPl78 peptides. The method is useful for identifying compounds, including
XX CC small molecule compounds, which may themselves exhibit antifusogenic,
XX CC antiviral or intracellular modulatory activity. The DPl78-like/DPl07-like
XX CC peptides are useful to inhibit human and non-human retroviral,
XX CC particularly HIV, transmission to uninfected cells. The present sequence
XX CC represents a peptide sequence from Staphylococcus aureus enterotoxin A
XX SQ Sequence 257 AA;
Query Match 82.6%; Score 1023; DB 4; Length 257;
Best Local Similarity 82.0%; Pred. No. 3.5e-94;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
Qy 1 SEKSEINEKDLRKSELRNALSLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
Db 25 SEKSEINEKDLRKSELRQGTALGNLQIYYNEKAKTENKESHDPQLQHTILFKGFTD 84
Qy 61 HPWYNDLLVLDGSDATNKYKGGKVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDI VDKYKGGKVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPLETVTKNKKVTVQELDLQARHYLHGKFLYNSDSFGGKVQ 204
Qy 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNKTINSENHLDIYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHLDIYLTS 257


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RESULT 19
ABO10269
ID ABO10269 standard; protein; 257 AA.
XX
AC ABO10269;
XX
DT 19-AUG-2003 (first entry)
XX
DE S. aureus enterotoxin A.
XX
KW HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
KW Epstein-Barr virus infection; heptad repeat motif.
XX
OS Staphylococcus aureus.
XX
PN US6518013-B1.
XX
PD 11-FEB-2003.
XX
PF 07-JUN-1995; 95US-00485546.
XX
PR 07-JUN-1993; 93US-00073028.
PR 07-JUN-1994; 94US-00255208.
PR 20-DEC-1994; 94US-00360107.
XX
PA (TRIM-) TRIMERIS INC.
XX
PI Barney SO, Lambert DM, Petteway SR;
PI WPI; 2003-465599/44.
XX
DR Inhibiting transmission of Epstein-Barr virus to a cell, by contacting
DR the cell with a peptide consisting of a region of Epstein-Barr virus
XX protein.
XX Example; Fig 42; 716pp; English.
XX
CC The invention relates to inhibiting (M) transmission of an Epstein-Barr
CC virus to a cell, comprising contacting the cell with an effective
CC concentration of a peptide consisting of a region of 16-39 consecutive
CC amino acids of an Epstein-Barr virus protein for an effective period of
CC time, where the region is recognised by one or more of ALIMOTIS,
CC 107x178x4 or PLZIP sequence search motifs, the peptide further comprises
CC an amino terminal X, and a carboxy terminal Z in which X comprises an
CC amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic
CC group or macromolecular carrier group, and Z comprises a carboxyl group,
CC amide group, hydrophobic group, or macromolecular carrier group, and
CC fusion of the virus to the cell is inhibited. The peptides were
CC identified by analysing the structure/motifs present in the HIV-1
CC glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat
CC motif containing peptides were used to design the motifs cited above,
CC which in turn were used to analyse proteins from other pathogenic
CC organisms and HIV isolates, looking for DP107/178 structural analogues.
CC The method is useful for inhibiting transmission of Epstein-Barr virus to
CC a cell and Epstein-Barr virus infection. The present sequence is a
CC protein from a pathogenic organism analysed for regions analogous to
CC DP107 or DP178
XX
SQ Sequence 257 AA;

Query Match 82.6%; Score 1023; DB 6; Length 257;
Best Local Similarity 82.0%; Pred. No. 3.5e-94;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQNALSNLRQIYYNKEAITENKESDDQPLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOQNALSNLRQIYYNKEAITENKESDDQPLENTLLFKGFFTG 84

QY 61 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDLFDSDKIDVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

RESULT 20
ADD44368
ID ADD44368 standard; protein; 257 AA.
XX
AC ADD44368;
XX
DT 15-JAN-2004 (first entry)
XX
DE Staphylococcus aureus enterotoxin A protein.
XX
KW enterotoxin A; ent A; food poisoning; bacterium; food; milk; fruit juice;
KW ice cream.
XX
OS Staphylococcus aureus.
XX
PN WO2003080865-A1.
XX
PD 02-OCT-2003.
XX
PF 26-MAR-2002; 2002WO-IB001150.
XX
PR 26-MAR-2002; 2002WO-IB001150.
XX
PA (COUL ) COUNCIL SCI & IND RES.
XX
PI Padmapriya BP, Ramesh A, Chandrashekar A, Varadaraj MC;
XX WPI; 2003-779273/73.
XX N-PSDB; ADD44369.
XX
DR Novel oligonucleotide primers directed against enterotoxin A gene of
XX Staphylococcus aureus and heat stable enterotoxin gene of Yersinia
XX enterocolitica, useful for detecting food poisoning causing bacteria.
XX Example 2; Page 14-15; 34pp; English.
XX
CC The invention relates to novel oligonucleotide primers directed against
CC enterotoxin A gene (ent A) of Staphylococcus aureus and heat stable
CC enterotoxin gene (yst) of Yersinia enterocolitica. The novel
CC oligonucleotide primers are useful for simultaneously detecting food
CC poisoning bacterial species Staphylococcus aureus and/or Yersinia
CC enterocolitica in food systems e.g., milk, fruit juices and ice creams,
CC without prior enrichment for preventing food poisoning outbreak. The PCR
CC detection method is useful for detecting the bacteria strains in quantity
CC as low as one cell. The method can be directly used for detecting
CC bacterial strains. The oligonucleotide primers allow quick and highly
CC sensitive detection of the food poisoning bacterial species. This
CC sequence represents the protein derived from the enterotoxin A gene from
CC Staphylococcus aureus of the invention.
XX
SQ Sequence 257 AA;

Query Match 82.6%; Score 1023; DB 7; Length 257;
Best Local Similarity 82.0%; Pred. No. 3.5e-94;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQNALSNLRQIYYNKEAITENKESDDQPLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOQNALSNLRQIYYNKEAITENKESDDQPLENTLLFKGFFTG 84

QY 61 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDLFDSDKIDVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

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Qy	121	EKKVPINLWDGKQTTPIDIKVTSSKEVTVQELDLQARRHYLHGKFGLYNSDSFGGKVQ	180
Dd	145	EKKVPINLWLDGKONTVPLETNTKNKNTVQELDLQARRYLQEKYNLYNSDVPDGKVQ	204
Qy	181	RGLIVFHSSEGSTVSYDLFDAGQGYPDTLRLRIYRDNKTINSENHLIDLPLYTT	233
Dd	205	RGLIVFHTSTSPSYNDLDFGAQQGYSNLTLLRIYRDNKTINSNMHIDIPLYTS	257
 RESULT 21			
ADH10956			
ID	ADH10956	standard; protein; 257 AA.	
XX	AC	ADH10956;	
DT	11-MAR-2004	(first entry)	
XX	DE	Enterotoxin A protein.	
XX	KW	Enterotoxin A; Computational design; protein binding peptide;	
KW	KW	hydrophobic potential; solvent contact surface;	
KW	KW	protein three-dimensional structure; two-dimensional characteristic map;	
KW	KW	Fourier transformation.	
XX	OS	Staphylococcus aureus.	
XX	PN	JP2003263465-A.	
XX	PN	19-SEP-2003.	
XX	PF	07-MAR-2002; 2002JP-000623348.	
XX	PR	07-MAR-2002; 2002JP-000623348.	
XX	PA	(ENKA-) ENKAKU IRYO KENKYUSHO KK.	
XX	DR	WFI; 2004-075279/08.	
PT	PT	Designing and selecting protein binding peptide by identifying peptide	
PT	PT	binding region of protein, and designing peptides that bind to the region	
PT	PT	using structure-biological activity relationship program of computer.	
XX	PS	Example; SEQ ID NO 1; 1lpp; Japanese.	
XX	CC	The invention relates to a method for computational design and selection	
CC	CC	of protein binding peptides, comprising computing the hydrophobic	
CC	CC	potential of all surface points arranged on the solvent contact surface	
CC	CC	of a protein three-dimensional structure, developing a two-dimensional	
CC	CC	characteristic map by a self-assembly method, identifying a region of	
CC	CC	hydrophobic amino acids by Fourier transformation and designing a protein	
CC	CC	binding peptide corresponding to the hydrophobic region. The method is	
CC	CC	useful for designing and selecting protein binding peptides. This	
CC	CC	sequence represents an Enterotoxin A protein used in the scope of the	
CC	CC	invention.	
XX	Sequence	257 AA;	
SQ	Query Match	82.6%; Score 1023; DB 8; Length 257;	
	Best Local Similarity	82.0%; Pred. No. 3.5e-94;	
	Matches	191; Conservative 17; Mismatches 25; Indels 0; Gaps 0	
Qy	1	SEKSEEINEKDRLRKSELQRNALSNLRIOIYYNEKAITENKESDDQFLNTLLFKGFTG	60
Dd	25	SEKSEEINEKDRLRKSELQGTALGNLKQIYYNEKAKTENKESHDPQLQHTILFKGFETD	84
Qy	61	HPWYNDLLVDLGSDATNKYGKGKVDLYGAYVGOCAGTGNKTCMYGGVTLHDNNRLT	120
Dd	85	HSWYNDLLVDLFDSDKVIDVKYGGKGVKVDLYGAYVGOCAGTGNKTCMYGGVTLHDNNRLT	144
Qy	121	EKKVPINLWDGKQTTPIDIKVTSSKEVTVQELDLQARRHYLHGKFGLYNSDSFGGKVQ	180
Dd	145	EKKVPINLWLDGKONTVPLETNTKNKNTVQELDLQARRYLQEKYNLYNSDVPDGKVQ	204

Qy	181	RGLIVFHSSEGSTVSYDLFDAGQGVDPDTLLRIYRDNKTKINSENHLIDLYLXTT	233
Db	205	RGLIVFHTSTEPSVNYDLFGAQGVSNLTLLRIYRDNKTKINSENHIDIYLYTS	257
RESULT 22			
ID	AAW06738	AAW06738 standard; protein; 233 AA.	
XX	XX		
AC	AAW06738;		
DT	08-MAR-1997	(first entry)	
XX	XX		
DE	Staphylococcus enterotoxin A.		
XX	XX		
KW	Enterotoxin A; superantigen; antigen; cytokine; chemokine; T cell;		
KW	lymphocyte; monocyte; natural killer cell; gene therapy; cancer; vaccine;		
KW	adjuvant.		
XX	XX		
OS	Staphylococcus sp.		
XX	XX		
PN	W09636366-A1.		
XX	XX		
PD	21-NOV-1996.		
XX	XX		
PF	20-MAY-1996; 96WO-US007432.		
XX	XX		
PR	18-MAY-1995; 95US-00446918.		
PR	29-DEC-1995; 95US-00580806.		
XX	XX		
PA	(NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.		
XX	XX		
PI	Dow SW, Elmslie RE, Potter TA;		
XX	XX		
DR	WPI; 1997-011857/01.		
DR	N-PSDB; AAT45699.		
XX	XX		
PT	Recombinant molecule encoding super:antigen and opt. cytokine or		
PT	chemokine - controls activity of effector cells (T cells, monocytes,		
PT	natural killer cells), used for gene therapy of cancer.		
XX	XX		
PS	Example 1; Page 98-99; 131pp; English.		
XX	XX		
CC	A cDNA clone (AAT45699) codes for staphylococcal enterotoxin A (AAW06738)		
CC	superantigen. Nucleic acids encoding superantigens (see also AAW06737,		
CC	AAW06739), esp. truncated forms of the superantigen lacking the leader		
CC	peptide, can be used in the gene therapy of cancer, infectious diseases		
CC	and immunological disorders. The nucleic acid, optionally in combination		
CC	with cytokine or chemokine nucleic acids, is delivered to an animal using		
CC	e.g. liposomes. It acts by controlling the activity of effector cells,		
CC	such as T-cells, macrophages, monocytes and/or natural killer cells.		
CC	Localised prodn. of an effective but non-toxic amount of encoded proteins		
CC	allows safe treatment of the animal		
XX	XX		
SQ	Sequence 233 AA;		
Query Match 82.3%; Score 1019; DB 2; Length 233;			
Best Local Similarity 81.9%; Pred. No. 7,e-94;			
Matches 190; Conservative 17; Mismatches 25; Indels 0; Gaps 0			
Qy	2	EKSSEINEKDLRKSEIQRNALSNLRIYYINEKAITENKESDDQFLENTLLFKGFFTGH	61
Db	2	EKSSEINEKDLRKSEIQSGTALGNLQIYYINEKAKTENKESHDOFLOHTILFKGFFTDH	61
Qy	62	PWYNDLLVDLGSKDATNKYGGKGVLDLYGAYGYOCAGGTPNKTCAGYGGVTLHDNNRLTE	121
Db	62	SWYNDLLVDPSKDIVKYGKGVLDLYGAYGYOCAGGTPNKTCAGYGGVTLHDNNRLTE	121
Qy	122	EKKVPINLWDGKQTTVPIDPKVTSKKEVTVQELDQARHYLHGKFLYNSDSFGKQVOR	181
Db	122	EKKVPINLWDGKQNTVPLETVTKTNKNVTVQELDQARRYLQEKYINLYNSDVFDGKQVOR	181


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Db      61 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
      121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
      121 EEKVPINLWDGKQNTVPLETVTNKKNVTYQELDLQARRYLQEKYLYNSDVFDDGKVQ 180
      181 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRLRIYRDNKTINSENHLIDLYLTT 233
      181 RGLIVFHTSTEPSVNYDLFGAGQGYNTLLRIYRDNKTINSENMHIDIYLYTS 233

RESULT 25
AAB67338
ID AAB67338 standard; peptide; 233 AA.
XX
AC AAB67338;
XX
DT 23-APR-2001 (first entry)
XX
DE Staphylococcus aureus enterotoxin A protein.
XX
KW Tumour; cancer; immune; enterotoxin.
XX
OS Staphylococcus aureus.
XX
PN US6180097-B1.
XX
PD 30-JAN-2001.
XX
PF 30-OCT-1998; 98US-00183437.
XX
PR 03-OCT-1989; 89US-00416530.
XX
PR 17-JAN-1990; 90US-00466577.
XX
PR 17-JAN-1991; 91WO-00466577.
XX
PR 01-JUN-1992; 92US-00891718.
XX
PR 02-MAR-1993; 93US-00025144.
XX
PR 31-JAN-1994; 94US-00189424.
XX
PR 19-JUN-1995; 95US-00491746.
XX
PA (TERM/) TERMAN D S.
XX
PI Terman DS;
XX
DR WPI; 2001-158657/16.
XX
PT Tumor cell capable of stimulating antitumor immune reactivity in vitro or
PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
PT costimulatory molecule.
XX
PS Disclosure; Fig 2; 16pp; English.
XX
CC The present invention relates to a tumour cell capable of stimulating
CC antitumor immune reactivity in vitro or in vivo contains and expresses an
CC exogenous nucleic acid molecule encoding a superantigen or its active
CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
CC molecule that activates T cells in conjunction with an antigenic
CC stimulus. The invention may be used for cancer therapy by stimulating an
CC anticancer immune response in vivo or ex vivo
XX
SQ Sequence 233 AA;
      Query Match      82.1%; Score 1016; DB 4; Length 233;
      Best Local Similarity 81.5%; Pred. No. 1.5e-93;
      Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

Qy      1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNKEAITEKESDDQFLNTLLFKGFPTG 60
      1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNKEAKTENKESHQDQLHTILFKGFPTD 60
      61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
      61 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120

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Qy      121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
      121 EEKVPINLWDGKQNTVPLETVTNKKNVTYQELDLQARRYLQEKYLYNSDVFDDGKVQ 180
      181 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRLRIYRDNKTINSENHLIDLYLTT 233
      181 RGLIVFHTSTEPSVNYDLFGAGQGYNTLLRIYRDNKTINSENMHIDIYLYTS 233

RESULT 26
AAR45011
ID AAR45011 standard; protein; 233 AA.
XX
AC AAR45011;
XX
DT 25-MAR-2003 (revised)
DT 08-JUN-1994 (first entry)
XX
DE Staphylococcal enterotoxin SEA.
XX
KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KW autoimmune disease; toxicity; Protein A; perfusion system.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Misc-difference 49 /note= "Given in the specification as O, no further
FT details given"
XX
PN WO9324136-A1.
XX
PD 09-DEC-1993.
XX
PF 01-JUN-1993; 93WO-US005213.
XX
PR 01-JUN-1992; 92US-00891718.
XX
PA (TERM/) TERMAN D S.
PA (STON/) STONE J L.
XX
PI Terman DS, Stone JL;
XX
DR WPI; 1993-405418/50.
XX
PT Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
PT in a patient or for the treatment of auto-immune diseases.
XX
PS Disclosure; Fig 1; 90pp; English.
XX
CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer in
CC a patient. These SEs, and homologues of them, can be used as tumouricidal
CC agents for treating cancers and autoimmune disease. They exhibit
CC tumouricidal activity and toxicity identical to that observed for the
CC protein A perfusion system. They may be administered by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 233 AA;
      Query Match      81.8%; Score 1013; DB 2; Length 233;
      Best Local Similarity 81.5%; Pred. No. 3.1e-93;
      Matches 190; Conservative 16; Mismatches 27; Indels 0; Gaps 0;

Qy      1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNKEAITEKESDDQFLNTLLFKGFPTG 60
      1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNKEAKTENKESHQDQLHTILFKGFPTD 60
      61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
      61 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120

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XX Key Location/Qualifiers
FH Peptide 1..25
FT /label= Signal_peptide
FT Protein 25..257
FT /label= Mature_protein
FT Misc-difference 72
FT /note= "wild-type Leu substituted by Arg"
FT Misc-difference 94
FT /note= "wild-type Asp substituted by Arg"
FT Misc-difference 116
FT /note= "wild-type Tyr substituted by Ala"
XX
XX US6399332-B1.
PN
XX
PD 04-JUN-2002..
XX
XX 01-SEP-1998; 98US-00144776..
XX
XX 25-JUN-1997; 97US-00882431..
XX
XX (USSA ) US SEC OF ARMY.
XX
XX Ulrich RG, Olson MA, Bavari S;
XX
XX WPI; 2002-546281/58.
XX N-PSDB; ABN84222.
XX
XX Novel isolated and purified superantigen toxin DNA fragment which has
XX been genetically altered, useful for producing vaccine for treatment of
XX superantigen toxin-associated bacterial diseases.
XX
XX Claim 4; Col 33-35; 46pp; English.
XX
XX The present sequence is the protein sequence of staphylococcal
XX enterotoxin A (SEA) vaccine, periplasmic (A489270P). The vaccine
XX comprises 3 amino acid substitutions introduced into the SEA sequence:
XX L48R, Y69A and D70R. These mutations reduce the binding of the toxin to
XX major histocompatibility complex (MHC) Class II and/or T cell receptors.
XX The full-length expressed product is secreted into the periplasmic space
XX of Escherichia coli host cells, and the leader peptide is recognised and
XX cleaved by a native mechanism. The vaccine is used to protect against
XX the altered superantigen toxins as vaccines, and in diagnosis and
XX the superantigen is effectively recognised by the immune system and an
XX appropriate antibody response is produced. In examples from the
XX invention, attenuated superantigen toxins were shown to protect animals
XX against challenge with wild-type toxin. Methods of producing and using
XX the altered superantigen toxins as vaccines, and in diagnosis and
XX therapy, are provided. A multivalent vaccine consisting of altered
XX superantigen toxins from SEA, SEB, SEC-1, TSST-1 and streptococcal SPEA
XX is predicted to provide protective immunity against the majority of
XX bacterial superantigen toxins
XX
XX Sequence 257 AA;
XX
XX Query Match 80.8%; Score 1000; DB 5; Length 257;
XX Best Local Similarity 80.7%; Pred. No. 7.2e-92;
XX Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;
XX
XX 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLIFKGFFTG 60
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 25 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLIFKGFFTD 84
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMGVGLHDDNNRLT 120
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 85 HSWYNDLLVRFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMGVGLHDDNNRLT 144
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVK 180
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 145 EEKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARHYLHGKFGLYNSDSFGKVK 204
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 181 RGLIVFHSSEGSTSVSYDLFQAQQYSNTLLRIYRDNKTINSENHIDLYLYTT 233
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 205 RGLIVFHTSTEPSVNYDLFQAQQYSNTLLRIYRDNKTINSENHIDLYLYTS 257
RESULT 31
ABU10081
ID ABU10081 standard; protein; 257 AA.
XX
XX AC ABU10081;
XX
XX DT 11-AUG-2003 (first entry)
XX
XX DE Staphylococcal enterotoxin A #1.
XX
XX Enterotoxin A; superantigen-associated bacterial infection; vaccine;
XX superantigen toxin.
XX
XX OS Staphylococcus sp.
XX
XX PN US2003009015-A1;
XX
XX PD 09-JAN-2003.
XX
XX PF 25-JUN-1997; 97US-00882431.
XX
XX PR 25-JUN-1997; 97US-00882431.
XX
XX (ULRI/) ULRICH R G.
XX (OLSO/) OLSON M A.
XX (BAVA/) BAVARI S.
XX
XX Ulrich RG, Olson MA, Bavari S;
XX
XX WPI; 2003-401542/38.
XX N-PSDB; ACA61177.
XX
XX New superantigen toxin and/or DNA fragment with an altered binding of the
XX encoded altered toxin to either MHC class II or T cell antigen receptor,
XX useful for treating or ameliorating superantigen-associated bacterial
XX infection.
XX
XX Claim 10; Page 18-19; 50pp; English.
XX
XX The invention relates to an isolated and purified superantigen toxin
XX and/or DNA fragment, which has been altered so that the binding of the
XX encoded toxin to either major histocompatibility complex (MHC) class II
XX or T cell antigen receptor is altered. The superantigen toxins, DNA
XX fragments, and vaccines are useful for treating or ameliorating
XX superantigen-associated bacterial infection. The DNA fragments are
XX particularly useful for producing vaccine against superantigen toxin
XX infections. The transformed host cells are useful for analysing the
XX effectiveness of drugs and agents that affect the binding of
XX superantigens to MHC class II or T-cell antigen receptors. The present
XX sequence represents the amino acid sequence of staphylococcal enterotoxin
XX A #1
XX
XX Sequence 257 AA;
XX
XX Query Match 80.8%; Score 1000; DB 6; Length 257;
XX Best Local Similarity 80.7%; Pred. No. 7.2e-92;
XX Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;
XX
XX 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLIFKGFFTG 60
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 25 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFROHTILFKGFFTD 84
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMGVGLHDDNNRLT 120
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 85 HSWYNDLLVRFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMGVGLHDDNNRLT 144
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVK 180
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 145 EEKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARHYLHGKFGLYNSDSFGKVK 204
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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QY 181 RGLIVFHSSEGSTVSYDLFDAGQGVPTLLRIYRDNKTINSENHIDILYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGVSNLTLLRIYRDNKTINSENHIDILYLYTS 257

RESULT 32
ID ABU62324 standard; protein; 257 AA.

AC ABU62324;
XX
DT 27-AUG-2003 (first entry)
XX
DE S. aureus periplasmic enterotoxin A mutant #1.
KW SEA; staphylococcal enterotoxin A; mutein; mutant; vaccine;
KW superantigen toxin; MHC; superantigen-associated bacterial infection;
KW bacterial infection; antibacterial.
XX
OS Staphylococcus aureus.
OS Synthetic.

XX Key Location/Qualifiers
FH Peptide 1..24
FT /label= Signal_peptide
FT Protein 25..257
FT /label= Mature_SEA_mutant #1
FT Misc-difference 66 /note= "Wild-type Leu substituted by Glu"
FT Misc-difference 72 /note= "Wild-type Leu substituted by Arg"
FT Misc-difference 94 /note= "Wild-type Asp substituted by Arg"
FT Misc-difference 113 /note= "Wild-type Tyr substituted by Gly"
FT Misc-difference 116 /note= "Wild-type Tyr substituted by Ala"
XX

PN US2003036644-A1.
XX
PD 20-FEB-2003.
XX
XX 26-NOV-2001; 2001US-00002784.
XX
XX 25-JUN-1997; 97US-00882431.
PR 01-SEP-1998; 98US-00144776.
XX
XX (ULRI/) ULRICH R G.
PA
XX
XX Ulrich RG;
XX
XX WPI; 2003-492125/46.
DR N-PSDB; ACD28894.
XX
XX New superantigen toxin DNA fragment, useful for preparing a composition
PT for treating or preventing bacterial infection.
XX
XX Disclosure; Page 22-23; 68pp; English.

XX The invention relates to an isolated and purified superantigen toxin DNA
CC fragment is altered so that binding of the encoded altered toxin to
CC either the MHC class II or T cell antigen receptor is altered. Also
CC included are a recombinant DNA construct (comprising a vector and an
CC isolated and purified altered superantigen toxin DNA fragment), a host
CC cell transformed with the recombinant DNA construct, producing altered
CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
CC infection, a vaccine (comprising an altered superantigen toxin for
CC producing antigenic and immunogenic response resulting in the protection
CC of a mammal against superantigen-associated bacterial infection),
CC treating/ameliorating a superantigen-associated bacterial infection, an
CC antiserum isolated from individuals immunised with one or more altered
CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-

CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
CC SPEb). The superantigen toxin DNA fragment is useful for preparing a
CC composition for treating or preventing bacterial infection. The present
CC sequence represents the L42E/L48R/D70R/Y89G/Y92A (with reference to the
CC mature protein sequence) mutant of periplasmic SEA
XX
SQ Sequence 257 AA;

Query Match 80.8%; Score 1000; DB 7; Length 257;
Best Local Similarity 80.7%; Pred. No. 7.2e-92;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELRNALSNLRQIYYNEKATENKESDDQFLENTLLFKGFTG 60
DB 25 SEKSEINEKDLRKSELRNALSNLRQIYYNEKATENKESDDQFLENTLLFKGFTG 84
QY 61 HPWYNDLLVLDGSKDATNKYKGVLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVRFDSKDI VDKYKGVLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAGQGVPTLLRIYRDNKTINSENHIDILYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGVSNLTLLRIYRDNKTINSENHIDILYLYTS 257

RESULT 33
AAE37676
ID AAE37676 standard; protein; 257 AA.

AC AAE37676;
XX
DT 06-OCT-2003 (first entry)
XX
DE Protein #1 related to the invention.
KW Superantigen toxin; vaccine; infection; gene therapy.
XX
XX Unidentified.
XX WO2003056015-A1.
XX 10-JUL-2003.
XX
XX 26-NOV-2001; 2001WO-US046540.
XX
XX 26-NOV-2001; 2001US-00002784.
XX
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
PA
XX
XX Ulrich RG;
XX
XX WPI; 2003-492125/46.
DR N-PSDB; RAD56764.
XX

XX New superantigen toxin DNA fragment, useful for preparing a composition
PT for treating or preventing bacterial infection.
XX
XX Disclosure; Page 108-109; 141pp; English.
XX The invention provides a superantigen toxin DNA fragment which has been
CC genetically altered such that binding of the encoded altered toxin to
CC either the MHC class II or T cell antigen receptor is disrupted or
CC altered. DNA fragments of the invention are useful in the production of
CC vaccines against bacterial superantigen toxin infections. They are also
CC useful in gene therapy. The present sequence is a protein related to the
CC invention
XX
SQ Sequence 257 AA;

DR N-FSDB; ABN84223.
XX Novel isolated and purified superantigen toxin DNA fragment which has
PT been genetically altered, useful for producing vaccine for treatment of
PT superantigen toxin-associated bacterial diseases.
XX
PS Claim 5; Col 37-39; 46pp; English.
XX
XX The present sequence is the protein sequence of staphylococcal
CC enterotoxin A (SEA) vaccine, cytoplasmic (A489270C). The vaccine
CC comprises 3 amino acid substitutions introduced into the SEA sequence:
CC L48R, Y89A and D70R. These mutations reduce the binding of the toxin to
CC major histocompatibility complex (MHC) Class II and/or T cell receptors.
CC The protein is expressed as a nonsecreted product within host Escherichia
CC coli cells. The vaccine is used to protect against superantigen toxin
CC infections. Superantigen attributes are absent, but the superantigen is
CC effectively recognised by the immune system and an appropriate antibody
CC response is produced. In examples from the invention, attenuated
CC superantigen toxins were shown to protect animals against challenge with
CC wild-type toxin. Methods of producing and using the altered superantigen
CC toxins as vaccines, and in diagnosis and therapy, are provided. A
CC multivalent vaccine consisting of altered superantigen toxins from SEA,
CC SEB, SEC-1, TSS1-1 and streptococcal SPEa is predicted to provide
CC protective immunity against the majority of bacterial superantigen toxins
XX
SQ Sequence 233 AA;

Query Match 80.5%; Score 996; DB 5; Length 233;
Best Local Similarity 80.6%; Pred. No. 1.6e-91;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGH 61
DB 2 EKSEINEKDLRKSELQGTALGNLQIYYNEKAKTENKESHQDFRHTILFKGFFTDH 61

QY 62 PWYNDLLVLDGSKDATNKYKGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVRFDKDIIVDKYKGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121

QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVOR 181
DB 122 EKKVPINLWLDGKQNTVPLETVTKNKNVTVOELDLQARRYLQEKYNYLNSDVFQKQVOR 181

QY 182 GLIVFHSSEGSTVSVDLFDAGQOYPTLLRIYRDNKTINSENHLHDLYLTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAQOYSNTLLRIYRDNKTINSENHMDIYLYTS 233

RESULT 36
ABU10082
ID ABU10082 standard; protein; 233 AA.
XX ABU10082;
XX
XX 11-AUG-2003 (first entry)
XX
XX Staphylococcal enterotoxin A #2.
XX
XX Enterotoxin A; superantigen-associated bacterial infection; vaccine;
KW superantigen toxin.
XX
XX Staphylococcus sp.
XX
XX Key Location/Qualifiers
FH Misc-difference 1
FT /note= "Encoded by AT"
XX
XX US2003009015-A1.
XX
XX 09-JAN-2003.
XX
XX 25-JUN-1997; 97US-00882431.
XX

PR 25-JUN-1997; 97US-00882431.
XX (ULRI/) ULRICH R. G.
PA (OLSO/) OLSON M. A.
PA (BAVA/) BAVARI S.
XX
PI Ulrich RG, Olson MA, Bavari S;
XX
XX WPI; 2003-401542/38.
DR N-FSDB; ACA61178.
XX
XX New superantigen toxin and/or DNA fragment with an altered binding of the
PT encoded altered toxin to either MHC class II or T cell antigen receptor,
PT useful for treating or ameliorating superantigen-associated bacterial
PT infection.
XX
XX Claim 11; Page 20-21; 50pp; English.
PS
XX The invention relates to an isolated and purified superantigen toxin
CC and/or DNA fragment, which has been altered so that the binding of the
CC encoded toxin to either major histocompatibility complex (MHC) class II
CC or T cell antigen receptor is altered. The superantigen toxins, DNA
CC fragments, and vaccines are useful for treating or ameliorating
CC superantigen-associated bacterial infection. The DNA fragments are
CC particularly useful for producing vaccine against superantigen toxin
CC infections. The transformed host cells are useful for analysing the
CC effectiveness of drugs and agents that affect the binding of
CC superantigens to MHC class II or T-cell antigen receptors. The present
CC sequence represents the amino acid sequence of staphylococcal enterotoxin
CC A #2
XX
SQ Sequence 233 AA;

Query Match 80.5%; Score 996; DB 6; Length 233;
Best Local Similarity 80.6%; Pred. No. 1.6e-91;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGH 61
DB 2 EKSEINEKDLRKSELQGTALGNLQIYYNEKAKTENKESHQDFRHTILFKGFFTDH 61

QY 62 PWYNDLLVLDGSKDATNKYKGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVRFDKDIIVDKYKGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121

QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVOR 181
DB 122 EKKVPINLWLDGKQNTVPLETVTKNKNVTVOELDLQARRYLQEKYNYLNSDVFQKQVOR 181

QY 182 GLIVFHSSEGSTVSVDLFDAGQOYPTLLRIYRDNKTINSENHLHDLYLTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAQOYSNTLLRIYRDNKTINSENHMDIYLYTS 233

RESULT 37
ABU62325
ID ABU62325 standard; protein; 233 AA.
XX ABU62325;
XX
XX 27-AUG-2003 (first entry)
XX
XX S. aureus cytoplasmic enterotoxin A mutant #1.
XX
XX SEA; staphylococcal enterotoxin A; mutein; mutant; vaccine;
KW superantigen toxin; MHC; superantigen-associated bacterial infection;
KW bacterial infection; antibacterial.
XX
XX Staphylococcus aureus.
OS Synthetic.
OS
XX Key Location/Qualifiers
FH Misc-difference 1. .2
FT


```
RESULT 39
ID ABU10099 standard; protein; 233 AA.
XX
AC ABU10099;
XX
DT 11-AUG-2003 (first entry)
XX
DE Staphylococcus enterotoxin A K14E substitution mutant.
XX
KW Enterotoxin A; superantigen-associated bacterial infection; mutant;
KW superantigen toxin; vaccine; mutein.
XX
OS Staphylococcus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 14
FT /note= "Wild-type Lys substituted by Glu"
XX
PN US2003009015-A1.
XX
PD 09-JAN-2003.
XX
PF 25-JUN-1997; 97US-00882431.
XX
PR 25-JUN-1997; 97US-00882431.
XX
PA (ULRI/) ULRICH R G.
PA (OLSO/) OLSON M A.
PA (BAVA/) BAVARI S.
XX
PI Ulrich RG, Olson MA, Bavari S;
XX
DR WPI; 2003-401542/38.
XX
PT New superantigen toxin and/or DNA fragment with an altered binding of the
PT encoded altered toxin to either MHC class II or T cell antigen receptor,
PT useful for treating or ameliorating superantigen-associated bacterial
PT infection.
XX
PS Example 7; Page; 50pp; English.
XX
CC The invention relates to an isolated and purified superantigen toxin
CC and/or DNA fragment, which has been altered so that the binding of the
CC encoded toxin to either major histocompatibility complex (MHC) class II
CC or T cell antigen receptor is altered. The superantigen toxins, DNA
CC fragments, and vaccines are useful for treating or ameliorating
CC superantigen-associated bacterial infection. The DNA fragments are
CC particularly useful for producing vaccine against superantigen toxin
CC infections. The transformed host cells are useful for analysing the
CC effectiveness of drugs and agents that affect the binding of
CC superantigens to MHC class II or T-cell antigen receptors. The present
CC sequence represents the amino acid sequence of the staphylococcus
CC enterotoxin A K14E mutant. Note: The present sequence is not present in
CC the specification but was created by the indexer from the wild-type
CC staphylococcus enterotoxin A sequence (see ACA61178)
XX
SQ Sequence 233 AA;
Query Match 80.1%; Score 992; DB 6; Length 233;
Best Local Similarity 80.2%; Pred. No. 4e-91;
Matches 186; Conservative 18; Mismatches 28; Indels 0; Gaps 0;
QY 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 61
DB 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTDH 61
QY 62 PHYNLDLLVGLSGKDATNKKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLTE 121
DB 62 SWYNLDLLVRFDSKQIVTDYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARRHYLHGKFLGYNLSDSFGKQVR 181
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Db 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARRHYLHGKFLGYNLSDSFGKQVR 181
QY 182 GLIVFHSSEGSTVSVDLFDAGQGYPDTLRLRYRNKKTINSNLHDLVLYTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAGQGYSNLTLRLRYRNKKTINSNMHIDIYLYTS 233
RESULT 40
ADF89824
ID ADF89824 standard; protein; 231 AA.
XX
AC ADF89824;
XX
DT 26-FEB-2004 (first entry)
XX
DE Staphylococcal enterotoxin A (SEA) superantigen.
XX
KW Superantigen; SAg; Staphylococcal enterotoxin; SE; SEA; cytostatic;
KW gene therapy; cancer.
XX
OS Staphylococcus sp.
XX
PN WO2003094846-A2.
XX
PD 20-NOV-2003.
XX
PF 08-MAY-2003; 2003WO-US014381.
XX
PR 08-MAY-2002; 2002US-0378988P.
PR 15-JUN-2002; 2002US-0389366P.
PR 28-AUG-2002; 2002US-0406697P.
PR 29-AUG-2002; 2002US-0406750P.
PR 01-OCT-2002; 2002US-0415310P.
PR 02-OCT-2002; 2002US-0415400P.
PR 09-JAN-2003; 2003US-0438686P.
XX
PA (TERM/) TERMAN D S.
XX
PI Terman DS;
XX
DR WPI; 2004-011997/01.
XX
PT Treating a subject with cancer or malignant diseases comprises
PT intratumoral, intrathecal or intracavitary administration of an amount of
PT a superantigen composition to the subject.
XX
PS Disclosure; SEQ ID NO 1; 91pp; English.
XX
CC The invention relates to treating a subject with cancer. The method
CC involves administering an amount of a superantigen (SAG) composition
CC comprising a molecule selected from: a native SAG protein; its
CC biologically active fragment or a biologically active homologue or a
CC biologically active fusion protein comprising the SAG or its fragment or
CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
CC exotoxin, Y. pseudotuberculosis SAG, Mycoplasma arthritides SAG and
CC Clostridium perfringens exotoxin. The method is useful in treating cancer
CC or malignant diseases such as malignant pleural effusion, ascites,
CC pericardial effusion or meningial carcinomatosis. The present sequence
CC represents a Staphylococcal enterotoxin A (SEA) superantigen.
XX
SQ Sequence 231 AA;
Query Match 80.0%; Score 991; DB 8; Length 231;
Best Local Similarity 80.3%; Pred. No. 5e-91;
Matches 187; Conservative 18; Mismatches 26; Indels 2; Gaps 1;
QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELQNGTA--GNKQIYYNEKAITENKESDDQFLENTLLFKGFFTD 58
QY 61 HPWYNLDLLVGLSGKDATNKKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
```

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Db 59 HSWYNDLLVDFDSKDIIVDKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 118
Qy 121 EKKKVPINLWIDGKOTTPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVVQ 180
Db 119 EKKKVPINLWIDGKONTVPLETVTKNKNVTQVELDLQARRYLQEKYKLYNSDVPDGGKVV 178
Qy 181 RGLIVFHSSEGSTSVSYDLFDAGQYPTDLLRIYRDNKTINSNLHIDLYLTT 233
Db 179 RGLIVFHTSTEPSVNYDLFGAQGYSTNLLRIYRDNKINSNMHIDIYLYTS 231

RESULT 41
ABU10098
ID ABU10098 standard; protein; 233 AA.
XX
AC ABU10098;
XX
DT 11-AUG-2003 (first entry)
XX
DE Staphylococcus enterotoxin A Y64A substitution mutant.
XX
KW Enterotoxin A; superantigen-associated bacterial infection; mutant;
KW superantigen toxin; vaccine; mutein.
XX
OS Staphylococcus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 64 /note= "Wild-type Tyr substituted by Ala"
FT
PN US2003009015-A1.
XX
XX 09-JAN-2003.
XX
XX 25-JUN-1997; 97US-00882431.
XX
XX 25-JUN-1997; 97US-00882431.
XX
XX (ULRI/) ULRICH R G.
XX (OLSO/) OLSON M A.
XX (BAVA/) BAVARI S.
XX
PI Ulrich RG, Olson MA, Bavari S;
XX
XX WPI; 2003-401542/38.
XX
XX New superantigen toxin and/or DNA fragment with an altered binding of the
XX encoded altered toxin to either MHC class II or T cell antigen receptor,
XX useful for treating or ameliorating superantigen-associated bacterial
XX infection.
XX
XX Example 7; Page; 50pp; English.
XX
XX The invention relates to an isolated and purified superantigen toxin
XX and/or DNA fragment, which has been altered so that the binding of the
XX encoded toxin to either major histocompatibility complex (MHC) class II
XX or T cell antigen receptor is altered. The superantigen toxins, DNA
XX fragments, and vaccines are useful for treating or ameliorating
XX superantigen-associated bacterial infection. The DNA fragments are
XX particularly useful for producing vaccine against superantigen toxin
XX infections. The transformed host cells are useful for analysing the
XX effectiveness of drugs and agents that affect the binding of
XX superantigens to MHC class II or T-cell antigen receptors. The present
XX sequence represents the amino acid sequence of the staphylococcus
XX enterotoxin A Y64A mutant. Note: The present sequence is not present in
XX the specification but was created by the indexer from the wild-type
XX staphylococcus enterotoxin A sequence (see ACA61178)
XX
SQ Sequence 233 AA;
```

Query Match

79.7%; Score 987; DB 6; Length 233;

```
Best Local Similarity 80.2%; Pred. No. 1.3e-90;
Matches 186; Conservative 17; Mismatches 29; Indels 0; Gaps 0;
Qy 2 EKSEINEKDLRKSELSQNALSNLRQIYYNYNEKAITENKESDDQFLENTLLFKGFFTGH 61
Db 2 EKSEINEKDLRKSELSQNALSNLRQIYYNYNEKAITENKESDDQFLENTLLFKGFFTGH 61
Qy 62 PWYNDLLVDSKDATNKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLTE 121
Db 62 SWANDLLVRFDSKDIIVDKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLTE 121
Qy 122 EKKVPINLWIDGKOTTPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVVQ 181
Db 122 EKKVPINLWIDGKONTVPLETVTKNKNVTQVELDLQARRYLQEKYKLYNSDVPDGGKVVQ 181
Qy 182 GLIVFHSSEGSTSVSYDLFDAGQYPTDLLRIYRDNKTINSNLHIDLYLTT 233
Db 182 GLIVFHTSTEPSVNYDLFGAQGYSTNLLRIYRDNKINSNMHIDIYLYTS 233

RESULT 42
AAV70102
ID AAV70102 standard; protein; 257 AA.
XX
AC AAV70102;
XX
DT 05-JUN-2000 (first entry)
XX
DE Staphylococcus enterotoxin A.
XX
KW Superantigen toxin; SAG; Staphylococcus enterotoxin A; SEA; cytostatic;
KW antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
KW antibody; toxoid; staphylococcus/streptococcus toxin; diagnosis;
KW treatment; superantigen-associated bacterial infection.
XX
OS Staphylococcus sp.
XX
FH Key Location/Qualifiers
FT Peptide 2..25 /label= Leader_peptide
FT Protein 26..253 /label= Mature Staphylococcus enterotoxin A
FT /note= "Includes transcription start site residue, Met"
FT Misc-difference 42 /note= "Encoded by TTG"
FT Misc-difference 125 /note= "Encoded by CCA"
FT
XX WO200009154-A1.
XX
XX 24-FEB-2000.
XX
XX 13-AUG-1998; 98WO-US016766.
XX
XX 13-AUG-1998; 98WO-US016766.
XX (REED-) REED ARMY INST RES WALTER.
XX
XX Ulrich RG, Olson MA, Bavari S;
XX
XX WPI; 2000-224177/19.
XX N-PSDB; AA251105.
XX
XX Nucleic acid encoding superantigen toxin useful as a vaccine and for
XX diagnosis of superantigen-associated bacterial infections.
XX
XX Claim 7; Page 72-73; 118pp; English.
XX
XX The present amino acid sequence is the Staphylococcus enterotoxin A
XX (SEA), a bacterial superantigen toxin (SAG). The coding region of the SAG
XX toxin when altered by site directed mutagenesis, results in disruption of
XX binding of the toxin to both the MHC class II or T-cell antigen receptor.
XX SEA has antibacterial and cytostatic activity. This sequence is useful
```

CC for the production of SEA vaccines and specific antibodies. This vaccine
CC overcomes the disadvantages of the chemically inactivated toxins and is
CC designed to protect individuals against one or several related
CC staphylococcal and streptococcal toxins. It is used for the diagnosis and
CC treatment or amelioration of superantigen- associated bacterial
CC infections
XX
SQ Sequence 257 AA;

Query Match 79.4%; Score 983; DB 3; Length 257;
Best Local Similarity 79.8%; Pred. No. 3.7e-90;
Matches 186; Conservative 17; Mismatches 30; Indels 0; Gaps 0;
Qy 1 SEKSEINEKDLRKSELRNALSRLQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
Db 25 SEKSEINEKDLRKSEKQGTALGNLQIYYNEKAITENKESDDQFQHTILFKGFTD 84
Qy 61 HPWYNDLLVLDGSKDNTNKKYKGGVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVLPDSKDI VDKYKGGVDLYGAYAGYQCAGGTGNKTCMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKOTTPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKQV 180
Db 145 EEKVPINLWLDGKQNTVPLETVKTKNKNVTQVELDLQARHYLQEKYLNLYNSDVPDGKQV 204
Qy 181 RGLIVFHTSSEGSTVSYDLFDAQQGVPDILLRIYRDNKTINSENHIDLILYLYTT 233
Db 205 RGLIVFHTSTSPSVNYDLFGAQQGYSNTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 43
AAAY70103
ID AAAY70103 standard; protein; 233 AA.
XX
AC AAAY70103;
XX
DT 05-JUN-2000 (first entry)
XX
DE Mutant Staphylococcal enterotoxin A for vaccine A489270P.
XX
KW Superantigen toxin; SAG; Staphylococcal enterotoxin A; SEA; cytostatic;
KW antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
KW antibody; toxoid; staphylococcal/streptococcal toxin; diagnosis; mutant;
KW treatment; superantigen-associated bacterial infection; A489270P.
XX
OS Staphylococcus sp.
XX
FH Key Location/Qualifiers
FT Protein 1..233
FT /label= Mature Staphylococcal enterotoxin A
FT /note= "Mutant" sequence without the leader peptide"
FT Misc-difference 2
FT /note= "Encoded by AG"
FT Misc-difference 18
FT /note= "Encoded by TTG"
FT Misc-difference 48
FT /note= "Wild type Leu substituted with Arg"
FT Misc-difference 70
FT /note= "Wild type Asp substituted with Arg"
FT Misc-difference 92
FT /note= "Wild type Tyr substituted with Ala"
FT Misc-difference 157
FT /note= "Encoded by CTT"
FT Misc-difference 180
FT /note= "Encoded by CAG"
XX
PN WO200009154-A1.
XX
PD 24-FEB-2000.
XX
PF 13-AUG-1998; 98WO-US016766.
XX
PR 13-AUG-1998; 98WO-US016766.

XX
PA (REED-) REED ARMY INST RES WALTER.
XX
PI Ulrich RG, Olson MA, Bavari S;
XX
DR WPI; 2000-224177/19.
DR N-PSDB; AAZ51106.
XX
PT Nucleic acid encoding superantigen toxin useful as a vaccine and for
PT diagnosis of superantigen-associated bacterial infections.
XX
PS Claim 8; Page 74-76; 118pp; English.
XX
CC The present amino acid sequence is the mutant Staphylococcal enterotoxin
CC A (SEA), a bacterial superantigen toxin (SAG), used for the formulation
CC of SEA vaccine A489270P. The coding region of this SAG toxin is altered
CC by site directed mutagenesis, that results in disruption of binding of
CC the toxin to both the MHC class II or T-cell antigen receptor. This
CC altered SAG toxin has the leader peptide cleaved by native bacterial
CC enzymatic mechanism and the first residue of the mature protein is
CC encoded by the transcriptional start site (ATG). SEA has antibacterial
CC and cytostatic activity. This sequence is useful for the production of
CC SEA vaccines and specific antibodies. This vaccine overcomes the
CC disadvantages of the chemically inactivated toxins and is designed to
CC protect individuals against one or several related staphylococcal and
CC streptococcal toxins. It is used for the diagnosis and treatment or
CC amelioration of superantigen-associated bacterial infections
XX
SQ Sequence 233 AA;

Query Match 79.0%; Score 978; DB 3; Length 233;
Best Local Similarity 79.3%; Pred. No. 1e-89;
Matches 184; Conservative 17; Mismatches 31; Indels 0; Gaps 0;
Qy 2 EKSEINEKDLRKSELRNALSRLQIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
Db 2 EKSEINEKDLRKSEKQGTALGNLQIYYNEKAITENKESHDDQFQHTILFKGFTDH 61
Qy 62 PWYNDLLVLDGSKDNTNKKYKGGVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVLPDSKDI VDKYKGGVDLYGAYAGYQCAGTGNKTCMYGGVTLHDNNRLTE 121
Qy 122 EKKVPINLWIDGKOTTPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKQVOR 181
Db 122 EKKVPINLWLDGKQNTVPLETVKTKNKNVTQVELDKQARRYLQEKYLNLYNSDVPDGKVAR 181
Qy 182 GLIVFHSSEGSTVSYDLFDAQQGVPDILLRIYRDNKTINSENHIDLILYLYTT 233
Db 182 GLIVFHTSTSPSVNYDLFGAQQGYSNTLLRIYRDNKTINSENHIDIYLYTS 233

RESULT 44
ADF89835
ID ADF89835 standard; protein; 268 AA.
XX
AC ADF89835;
XX
DT 26-FEB-2004 (first entry)
XX
DE Staphylococcal enterotoxin J (SEJ) superantigen.
XX
KW Superantigen; SAG; Staphylococcal enterotoxin; SE; SEJ; cytostatic;
KW gene therapy; cancer.
XX
OS Staphylococcus sp.
XX
PN WO2003094846-A2.
XX
PD 20-NOV-2003.
XX
PF 08-MAY-2003; 2003WO-US014381.
XX
PR 08-MAY-2002; 2002US-0378988P.

Best Local Similarity 54.5%; Pred. No. 6e-58; Matches 126; Conservative 35; Mismatches 70; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNKAITENKESDDQFLENTLLPKGFTG 60
DB 26 NENIDSVKEKELHKSELSTALNNMKHSYADKNPIIGENKSTGDFLENTLLYKGFPTD 85
QY 61 HPWYNDLLVLDGSKDATNKGKVDLYGAYGYQCAGTPTNKACMYGGVTLHDNNRLT 120
DB 86 LINFEDLLINFNSKEMAQHFKSQNVDPYPIRYSINCYGGEIDRTACTYGGVTPHEGNK 145
QY 121 BEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 86 LINFEDLLINFNSKEMAQHFKSQNVDPYPIRYSINCYGGEIDRTACTYGGVTPHEGNK 145
QY 121 BEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 146 ERKKIPINLWINGVQKVSLOKVDKQNTVQELDAQARRYLOKDLKLYNNDLGGKIQ 205
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYQPTDLRIYRDNKTINSENHLIDILY 231
DB 206 RGKIEFSSDGSKVSYDLFDVKGDFPEKQLRIYSDNKTLSLSTHLHIDILY 256

RESULT 46
ADF43294
ID ADF43294 standard; protein; 258 AA.
XX AC ADF43294;
XX DT 12-FEB-2004 (first entry)
XX DE Staphylococcal enterotoxin D polypeptide seq id 14.
XX KW receptor; lipid-based tumour associated antigen; cytostatic;
XX KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
XX KW infectious disease; Staphylococcal enterotoxin D; SED; enterotoxin D.
XX OS Staphylococcus.
XX FN US2003157113-A1.
XX PD 21-AUG-2003.
XX PF 28-DEC-2000; 2000US-00751708.
XX PR 28-DEC-1999; 99US-0173371P.
XX PA (TERM/) TERMAN D S.
XX PI Terman DS;
XX DR WPI; 2003-787326/74.
XX PT New receptor in a mammalian cell that inhibits regular activation by
XX PT receptors specific for lipid-based tumor associated antigens, useful for
XX PT treating a neoplastic disease or tumor, and infectious diseases.
XX PS Example 3; SEQ ID NO 14; 151pp; English.
XX CC The invention describes a receptor in a mammalian cell that inhibits
XX CC regular activation by receptors specific for lipid-based tumour
XX CC associated antigen. The receptor has cytostatic and antimicrobial
XX CC properties and is suitable for use in gene therapy. The receptors,
XX CC methods and compositions are useful for treating a neoplastic disease or
XX CC tumour (cancer), and infectious diseases. This is the amino acid sequence
XX CC of an enterotoxin superantigen polypeptide the DNA encoding which can be
XX CC transfected in to a cell alone or with DNA encoding a cell surface moiety
XX CC to generate antitumour immunity.
XX SQ Sequence 258 AA;

Query Match 53.6%; Score 663; DB 7; Length 258;
Best Local Similarity 54.5%; Pred. No. 6e-58; Matches 126; Conservative 35; Mismatches 70; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNKAITENKESDDQFLENTLLPKGFTG 60

DB 26 NENIDSVKEKELHKSELSTALNNMKHSYADKNPIIGENKSTGDFLENTLLYKGFPTD 85
QY 61 HPWYNDLLVLDGSKDATNKGKVDLYGAYGYQCAGTPTNKACMYGGVTLHDNNRLT 120
DB 86 LINFEDLLINFNSKEMAQHFKSQNVDPYPIRYSINCYGGEIDRTACTYGGVTPHEGNK 145
QY 121 BEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 146 ERKKIPINLWINGVQKVSLOKVDKQNTVQELDAQARRYLOKDLKLYNNDLGGKIQ 205
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYQPTDLRIYRDNKTINSENHLIDILY 231
DB 206 RGKIEFSSDGSKVSYDLFDVKGDFPEKQLRIYSDNKTLSLSTHLHIDILY 256

RESULT 47
ADF9829
ID ADF9829 standard; protein; 258 AA.
XX AC ADF9829;
XX DT 26-FEB-2004 (first entry)
XX DE Staphylococcal enterotoxin D (SED) superantigen.
XX KW Superantigen; SAg; Staphylococcal enterotoxin; SE; SED; cytostatic;
XX KW gene therapy; cancer.
XX OS Staphylococcus sp.
XX FN WO2003094846-A2.
XX PD 20-NOV-2003.
XX PF 08-MAY-2003; 2003WO-US014381.
XX PR 08-MAY-2002; 2002US-0378988P.
XX PR 15-JUN-2002; 2002US-0389366P.
XX PR 28-AUG-2002; 2002US-0406697P.
XX PR 29-AUG-2002; 2002US-0406750P.
XX PR 01-OCT-2002; 2002US-0415310P.
XX PR 02-OCT-2002; 2002US-0415400P.
XX PR 09-JAN-2003; 2003US-0438686P.
XX PA (TERM/) TERMAN D S.
XX PI Terman DS;
XX DR WPI; 2004-011997/01.
XX PT Treating a subject with cancer or malignant diseases comprises
XX PT intratumoral, intrathecal or intracavitary administration of an amount of
XX PT a superantigen composition to the subject.
XX PS Disclosure; SEQ ID NO 6; 91pp; English.
XX CC The invention relates to treating a subject with cancer. The method
XX CC involves administering an amount of a superantigen (SAG) composition
XX CC comprising a molecule selected from: a native SAG protein; its
XX CC biologically active fragment or a biologically active homologue or a
XX CC biologically active fusion protein comprising the SAG or its fragment or
XX CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
XX CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
XX CC exotoxin, γ pseudocuberculosis SAG, Mycoplasma arthritis SAG and
XX CC Clostridium perfringens exotoxin. The method is useful in treating cancer
XX CC or malignant diseases such as malignant pleural effusion, ascites,
XX CC pericardial effusion or meningeal carcinomatosis. The present sequence
XX CC represents a Staphylococcal enterotoxin D (SED) superantigen.
XX SQ Sequence 258 AA;

Query Match 53.6%; Score 663; DB 8; Length 258;


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Query Match      53.1%; Score 657; DB 4; Length 228;
Best Local Similarity 55.6%; Pred. No. 2e-57;
Matches 125; Conserved 33; Mismatches 67; Indels 0; Gaps 0
QY 7 INEKDI RKSEIQRNALS NLRQIYYNEKATENKESDDQLENTILPKGFTCHPWND 66
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 VKSEIHKHKESEISSLTALNKHGYSADKPQIIGENKSTGDQLENTLLYKFFETLIINF 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 LLVDLGSKDQATNKYKGGKVDLYCAYYGQACAGTNPKTACMGVTLHNNRLTEEKVP 120

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Db 2 VKEKELHKKSELSSTALNNMKHSYADNP I I G E N K S T G D Q F L E N T L L Y K K F T D L I N F E D 61
QY 67 LLVDLGSKDATNKYKGGKVDLYGAYYGYOCAGGTPNKTA C M Y G G V T L H D N N R L T B E K K V P 126
Db 62 LLINFSKEMAHQFKSKNDVVPYPIRYSINCYGGEIDRTACTYGGVTPHEGKLEKERRKIP 121
QY 127 INLWIDGKTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVGQRLIVF 186
Db 122 INLWINGVQKESLDRKVDQKKNVTQELDAQARRYLOKDLKLYNNDTLGGKIQRGKIEF 181
QY 187 HSEGSTVSYDLFDAQGYQPTLLRIYRDNKTINSENHLHIDLVL 231
Db 182 DSSDGSKVSYDLFDVKGDFPEKQLRIYSNKTLSLHHLHIDLVL 226

RESULT 52
ABP58459
ID ABP58459 standard; protein; 203 AA.
AC ABP58459;
XX
DT 14-APR-2003 (first entry)
XX
DE Staphylococcal enterotoxin D.
XX
KW Superantigen; staphylococcal enterotoxin D; antibody; cancer; tumour;
KW cytostatic; vaccine.
XX
OS Staphylococcus sp.
XX
PN WO2003002143-A1.
XX
PD 09-JAN-2003.
XX
PF 19-JUN-2002; 2002WO-SE001188.
XX
PR 28-JUN-2001; 2001SE-00002327.
XX
PA (ACTI-) ACTIVE BIOTECH AB.
XX
PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
XX
DR WPI; 2003-201467/19.

Conjugate for therapy, has bacterial superantigen with a region in T-cell receptor and four regions to determine binding to class II major histocompatibility complex, antibody to cancer associated cell surface structure.

Example 3; Fig 3; 102pp; English.
The present sequence is the protein sequence of staphylococcal enterotoxin D (SED). The invention provides novel conjugates (see ABP58454) for human cancer therapy. These comprise an engineered bacterial superantigen, such as novel SEA/E-120 (see ABP58455), and an antibody moiety, such as tumour reactive antibody 574. Bacterial enterotoxins such as SEA, SEE, SED and SEH were used in the molecular modelling of the engineered superantigens. The superantigens were engineered to reduce seroreactivity whilst maintaining biological activity and production levels. The novel conjugates were designed to target and destroy cancer cells, including cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)

Sequence 203 AA;
Query Match 42.2%; Score 523; DB 6; Length 203;
Best Local Similarity 49.5%; Pred. No. 5.2e-44;
Matches 109; Conservative 25; Mismatches 66; Indels 20; Gaps 3;

QY 12 LRKSELOALNLRQIYYNEKAITENKESDDQFLENTLLFKGPTGHPWINDLIVDL 71
Db 2 LHKSELSSTALNNMKHSYADNP I I G E N K S T G D Q F L E N T L L Y K A P F -----LLINF 53

QY 72 GSKDATNKYKGGKVDLYGAYYGYOCAGGTPNKTA C M Y G G V T L H D N N R L T E E K K V P I N L W I 131
Db 54 NSAEHAQHFKSKNDVVPYAIRYAAAC-----RTACTYGGVTPHAGNALRKARKKIPINLWI 107
QY 132 DGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVGQRLIVFHSSEG 191
Db 108 IGQXEVSLDKVQTDKKNVTQELDAQARRYLOKDLKLYNA-----IQRGKLEFDSAAA 161
QY 192 STVSVDLFDQAQGYQPTLLRIYRDNKTINSENHLHIDLVL 231
Db 162 SKVSVDLFDVAGDFPEKQLRIYSNKTLSLHHLHIDLVL 201

RESULT 53
ABM70958
ID ABM70958 standard; protein; 250 AA.
XX
AC ABM70958;
DT 20-NOV-2003 (first entry)
XX
DE Staphylococcus aureus protein #198.
XX
KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
KW enzymatic assay; antibiotic target.
XX
OS Staphylococcus aureus.
XX
PN WO200294868-A2.
XX
PD 28-NOV-2002.
XX
PF 27-MAR-2002; 2002WO-IB002637.
XX
PR 27-MAR-2001; 2001GB-00007661.
XX
PA (CHTR-) CHIRON SPA.
XX
PI Masignani V, Mora M, Scarselli M;
XX
DR WPI; 2003-120786/11.
DR N-PSDB; ACF72518.

New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused by S. aureus, e.g. sepsis.

Claim 1; SEQ ID NO 396; 49pp; English.
The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention

Sequence 250 AA;
Query Match 39.8%; Score 492.5; DB 6; Length 250;
Best Local Similarity 39.8%; Pred. No. 8.3e-41;
Matches 92; Conservative 48; Mismatches 86; Indels 5; Gaps 3;

QY 1 SEKSEINEKDLRKKGSELOALNLRQIYYNEKAITENKESDDQFLENTLLFKGPTG 60
Db 23 TNSASAIETSYDLHKKSKFDSKRLSNAK-MSFINPTQL-ENKNTNDRLLKHDLFHDMFVN 80
QY 61 HPWINDLIVDLGSKDATNKYKGGKVDLYGAYYGYOCAGGTPNKTA C M Y G G V T L H D N N R L T 120
Db 81 DWMKDKPKEFENEALSKKPKINKDIDIFAGNYGCHGGATNKTQCSYGGVTLSDNNKYD 140

121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHVLHCKFGLYNSDSFGGKVKQ 180
141 DYKNIPCNLWIDGHQTELELTAVKTKKIVITQELEVLRNLYNEBKYLQEY---GGDIV 197
181 RGLIVFHSSEGSTVSYDLFDAGQGVPTDLRIYRDNKNTINSENLDILYLY 231
198 KGYYKVNDDSDONVEYDPYNLNGEGREVLKMYADKNTINSKLDLILYF 248

RESULT 54
ABU10091
ID ABU10091 standard; protein; 82 AA.
XX
XX AC ABU10091;
XX
XX
XX DT 11-AUG-2003 (first entry)
XX
XX Bacterial superantigen toxin SEE.
DE
XX Superantigen-associated bacterial infection; superantigen toxin; vaccine;
KW
KW SEE.

XX	Unidentified.	
OS		
XX		
XX	US2003009015-A1.	
XX		
XX		
XX	09-JAN-2003.	
XX		
XX		
XX		
XX	25-JUN-1997;	97US-00882431.
XX		
XX	25-JUN-1997;	97US-00882431.
XX		
XX	(ULRI/) ULRICH R G.	
PA	(OLSO/) OLSON M A.	
PA	(BAVA/) BAVARI S.	
PA		
XX		
PI	Ulrich RG,	Olson MA, Bavari S;
XX		
XX		
DR	WPI; 2003-401542/38.	

XX New superantigen toxin and/or DNA fragment with an altered binding of the
PT encoded altered toxin to either MHC class II or T cell antigen receptor,
PT useful for treating or ameliorating superantigen-associated bacterial
PT infection.
XX Example 1: Page 36; 50pp; English.

The invention relates to an isolated and purified superantigen toxin and/or DNA fragment, which has been altered so that the binding of the encoded toxin to either major histocompatibility complex (MHC) class II or T cell antigen receptor is altered. The superantigen toxins, DNA fragments, and vaccines are useful for treating or ameliorating superantigen-associated bacterial infection. The DNA fragments are particularly useful for producing vaccine against superantigen toxin infections. The transformed host cells are useful for analysing the effectiveness of drugs and agents that affect the binding of superantigens to MHC class II or T-cell antigen receptors. The present sequence represents the amino acid sequence of the bacterial superantigen toxin SEE

	SQ	Sequence	82 AA;
		Query Match Best Local Similarity Matches	36.9%; Score 457; DB 6; Length 82; 100.0%; Pred. No. 6.3e-38; 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	43	SDDQFLENTLLFKGFFTHPWNDLVLGSKDATNKYGGKVDLYGYAYGYQCAGGTN	102
Dd	1	SDDQFLENTLLFKGFFTHPWNDLVLGSKDATNKYGGKVDLYGYAYGYQCAGGTN	60
	103	KTACMYGVVTLHNDNNRLTEEEK	124

Dd	61	KTACMYGGVTILHDNNRLTEEK	82
RESULT 55			
ABU62338			
ID	ABU62338	standard; protein; 82 AA.	
XX	AC	ABU62338;	
XX	XX		
XX	XX	27-AUG-2003 (first entry)	
XX	XX		
XX	XX	S. aureus enterotoxin E, SEE, MHC binding region.	
XX	XX		
KW	SE	staphylococcal enterotoxin E; vaccine; superantigen toxin; MHC;	
KW	SE	superantigen-associated bacterial infection; bacterial infection;	
KW	SE	antibacterial.	
XX	XX		
OS	Staphylococcus aureus.		
XX	XX		
PN	US2003036644-A1.		
XX	XX		
PD	20-FEB-2003.		
XX	XX		
XX	XX	26-NOV-2001; 2001US-00002784.	
XX	XX		
PR	25-JUN-1997;	97US-00882431.	
PR	01-SEP-1998;	98US-00144776.	
XX	XX		
PA	(ULRI/) ULRICH R G.		
XX	XX		
XX	XX	Ulrich RG;	
XX	XX		
XX	XX	WPI; 2003-492125/46.	
XX	XX		
PT	XX	New superantigen toxin DNA fragment, useful for preparing a composition	
PT	XX	for treating or preventing bacterial infection.	
XX	XX		
PS	Disclosure; Fig 3: 68pp; English.		

The invention relates to an isolated and purified superantigen toxin DNA fragment is altered so that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is altered. Also included are a recombinant DNA construct (comprising a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, an altered TST-1 (toxic shock syndrome toxin) superantigen toxin peptide, diagnosing superantigen-associated bacterial infection, a vaccine (comprising an altered superantigen toxin for producing antigenic and immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection), treating/ameliorating a superantigen-associated bacterial infection, antiseria isolated from individuals immunised with one or more altered TST-1 superantigen toxin and an antibody which recognises altered TST-1 superantigen toxin.

1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA, SEB, SECI) and streptococcal pyrogenic enterotoxin a and b (SPAa and SPeb). The superantigen toxin DNA fragment is useful for preparing a composition for treating or preventing bacterial infection. The present sequence represents the *S. aureus* enterotoxin E, SEE, MHC binding region

Sequence 82 AA:

Query Match	36.9%	Score 457;	DB 7;	Length 82;
Best Local Similarity	100.0%;	Pred. No. 6.3e-38;		
Matches 82;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	43	SDQFLENTLLFKGFFTGHPWYNDLLVDLSKDATNKYKGGKVDLYGAYYGCACGGTPN	102	
Db	1	SDQFLENTLLFKGFFTGHPWYNDLLVDLSKDATNKYKGGKVDLYGAYYGCACGGTPN	60	
Qy	103	KTACWYGGVTLHDNNRLTEKK	124	
Db	61	KTACWYGGVTLHDNNRLTEKK	82	

DE Staphylococcus aureus Gene #5 polypeptide sequence 2.
XX Staphylococcus aureus WCUH 29; antagonist; antibacterial; immunogen;
KW vaccine; disease; protection; isolation.
XX Staphylococcus aureus.
OS
FH Key Location/Qualifiers
FT Misc-difference 29
TT /note= "Unspecified amino acid"
XX
FN WO9731114-A2.
XX
XX 28-AUG-1997.
PD
XX
PF 25-FEB-1997; 97WO-GB000524.
XX
PR 26-FEB-1996; 96GB-00004045.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Burnham MKR, Hodgson JE;
XX
XX WPI; 1997-435166/40.
DR N-PSDB; AAV01865.
XX
XX New Staphylococcus aureus polynucleotide and polypeptide(s) - for
PT isolating antagonist of the polypeptide(s) useful as anti-bacterials.
XX
XX Claim 11; Page 33; 117pp; English.
PS
XX The present sequence represents a novel polypeptide, which is optionally
CC expressed in NCIMB 40771. The polypeptide, and polynucleotide encoding
CC it, are derived from Staphylococcus aureus. Cells expressing ligands that
CC bind the polypeptide can be used to isolated candidate compounds that
CC bind and inhibit the activity of the polypeptide. Such compounds can be
CC used as anti-bacterial compounds. The polypeptide may also be used as an
CC immunogen to vaccinate an animal for protection against Staphylococcus
CC aureus caused disease
XX
SQ Sequence 91 AA;
Query Match 29.9%; Score 370; DB 2; Length 91;
Best Local Similarity 76.9%; Pred. No. 4.2e-29;
Matches 70; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
Qy 107 MYGGVTLHDNRLTEKKVQVPLNLWDGKQTTVPIDKVTSKVETVQELDLQARHYLHGK 166
Db 1 MYGGVTLHDNRLTEKKVQVPLNLWDGKQTTVPIDKVTSKVETVQELDLQARHYLHGK 60
Qy 167 FGLYNSDSFGKVGQVGLIVEHSSEGSTVSYD 197
Db 61 YNLVNSDVFDGKVGQVGLIVEHSTPVSVD 91
RESULT 59
ABP58460
ID ABP58460 standard; protein; 217 AA.
XX
AC ABP58460;
XX
XX 14-APR-2003 (first entry)
DT
XX Staphylococcal enterotoxin H.
DE Superantigen; staphylococcal enterotoxin H; antibody; cancer; tumour;
KW cytostatic; vaccine.
XX
XX Staphylococcus sp.
OS
XX WO20003002143-A1.
FN
XX 09-JAN-2003.
PD

XX 19-JUN-2002; 2002WO-SE001188.
PF
XX 28-JUN-2001; 2001SE-00002327.
PR
XX (ACTI-) ACTIVE BIOTECH AB.
PA
XX Forsberg G, Erlandsson E, Antonsson P, Walse B;
PI
XX WPI; 2003-201467/19.
DR
XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
PT receptor and four regions to determine binding to class II major
PT histocompatibility complex, antibody to cancer associated cell surface
PT structure.
XX
XX Example 3; Fig 3; 102pp; English.
PS
XX The present sequence is the protein sequence of staphylococcal
CC enterotoxin D (SED). The invention provides novel conjugates (see
CC ABP58454) for human cancer therapy. These comprise an engineered
CC bacterial superantigen, such as novel SEA/E-120 (see ABP58455), and an
CC antibody moiety, such as tumour reactive antibody 574. Bacterial
CC enterotoxins such as SEA, SEE, SED and SEH were used in the molecular
CC modelling of the engineered superantigens. The superantigens were
CC engineered to reduce seroreactivity whilst maintaining biological
CC activity and production levels. The novel conjugates were designed to
CC target and destroy cancer cells, including cancer of the lung, breast,
CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
XX
SQ Sequence 217 AA;
Query Match 29.6%; Score 366; DB 6; Length 217;
Best Local Similarity 37.9%; Pred. No. 3.6e-28;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;
Qy 10 KDLRKKSELQNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFTTGHPMVNDLLV 69
Db 1 EDLHDKSELTDALAN--AVGQYHPPFIKENIKSDEISGEKDLIFRN--QGDSEG-NDLRV 55
Qy 70 DLGSKDATNKYGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNRLTEKKVQVPLNL 129
Db 56 KFATADLAQKFKNNKNDIYGASFYKCEKISENISECLYGGTTL-NSEKLAQERVIGANV 114
Qy 130 WIDGKQTTVPIDKVTSKVETVQELDLQARHYLHGKFGLYNSDSFGKVGQVGLIVEHSS 189
Db 115 WVDGIQKETEL--IRTKKNVTLOELDIKIRKILSKDKYIKYKDS---EISKGLIEFDMK 169
Qy 190 EGSTVSYDLFDAQGYPTDLRLIYRDNKTINSENL-HIDLXYLT 232
Db 170 TPRDYSFDIYDLKGENDYEIDKIYEDNKTLSKDDSHIDVNLVT 213
RESULT 60
ADF89833
ID ADF89833 standard; protein; 217 AA.
XX
AC ADF89833;
XX
XX 26-FEB-2004 (first entry)
DT
XX Staphylococcal enterotoxin H (SEH) superantigen.
DE Superantigen; SAg; Staphylococcal enterotoxin; SE; SEH; cytostatic;
KW gene therapy; cancer.
XX
XX Staphylococcus sp.
OS
XX WO2003094846-A2.
FN
XX 20-NOV-2003.
PD
XX 08-MAY-2003; 2003WO-US014381.
PF

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XX PR 08-MAY-2002; 2002US-0378988P.
XX PR 15-JUN-2002; 2002US-0389366P.
XX PR 28-AUG-2002; 2002US-0406697P.
XX PR 29-AUG-2002; 2002US-0408750P.
XX PR 01-OCT-2002; 2002US-0415310P.
XX PR 02-OCT-2002; 2002US-0415400P.
XX PR 09-JAN-2003; 2003US-0438686P.
XX PA (TERM/) TERMAN D S.
XX PI Terman DS;
XX DR WPI; 2004-011997/01.
XX PT Treating a subject with cancer or malignant diseases comprises
XX PT intratumoral, intrathecal or intracavitary administration of an amount of
XX PT a superantigen composition to the subject.
XX PS Disclosure; SEQ ID NO 10; 91pp; English.
XX CC The invention relates to treating a subject with cancer. The method
XX CC involves administering an amount of a superantigen (SAG) composition
XX CC comprising a molecule selected from: a native SAG protein; its
XX CC biologically active fragment or a biologically active homologue or a
XX CC biologically active fusion protein comprising the SAG or its fragment or
XX CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
XX CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
XX CC exotoxin, Y. pseudotuberculosis SAg, Mycoplasma arthritides SAG and
XX CC Clostridium perfringens exotoxin. The method is useful in treating cancer
XX CC or malignant diseases such as malignant pleural effusion, ascites,
XX CC pericardial effusion or meningeal carcinomatosis. The present sequence
XX CC represents a Staphylococcal enterotoxin H (SEH) superantigen.
XX SQ Sequence 217 AA;
Query Match 29.6%; Score 366; DB 8; Length 217;
Best Local Similarity 37.9%; Pred. NO. 3.6e-28;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;
QY 10 KDLRKSELSORALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHPWYNDLAV 69
DB 1 EDLHDKSELTLALAN--AYGQYNHPFIKENIKSDEISGEKOLIFRN--QGDSG--NDLRV 55
QY 70 DLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGVTLDHNNRLTEKKVPINL 129
DB 56 KFATADLAOKFRKNVDIYGASFYKCEKISENISCLYGGTTL--NSEKLAQERVIGANV 114
QY 130 WIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVKQRLIVFHS 189
DB 115 WVDGIQKETEL--IRTNKNVTLQELDIKIRKILSDKIKYKDS---BISKGLIEFDMK 169
QY 190 EGSSTVSYDLFDAGQGVPTDLLRIYRDNKNTINSENH--HIDLYLT 232
DB 170 TPRDYSFDIYDLKGENDEYDKIYEDNKTLKSDSHIDVNLVT 213
RESULT 61
ADF89834
ID ADF89834 standard; protein; 242 AA.
XX AC ADF89834;
XX DT 26-FEB-2004 (first entry)
XX DE Staphylococcal enterotoxin I (SEI) superantigen.
XX KW Superantigen; SAG; Staphylococcal enterotoxin; SE; SEI; cytostatic;
XX KW gene therapy; cancer.
XX OS Staphylococcus sp.
XX PN WO2003094846-A2.

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XX PD 20-NOV-2003.
XX PF 08-MAY-2003; 2003WO-US014381.
XX PR 08-MAY-2002; 2002US-0378988P.
XX PR 15-JUN-2002; 2002US-0389366P.
XX PR 28-AUG-2002; 2002US-0406697P.
XX PR 29-AUG-2002; 2002US-0406750P.
XX PR 01-OCT-2002; 2002US-0415310P.
XX PR 02-OCT-2002; 2002US-0415400P.
XX PR 09-JAN-2003; 2003US-0438686P.
XX PA (TERM/) TERMAN D S.
XX PI Terman DS;
XX DR WPI; 2004-011997/01.
XX PT Treating a subject with cancer or malignant diseases comprises
XX PT intratumoral, intrathecal or intracavitary administration of an amount of
XX PT a superantigen composition to the subject.
XX PS Disclosure; SEQ ID NO 11; 91pp; English.
XX CC The invention relates to treating a subject with cancer. The method
XX CC involves administering an amount of a superantigen (SAG) composition
XX CC comprising a molecule selected from: a native SAG protein; its
XX CC biologically active fragment or a biologically active homologue or a
XX CC biologically active fusion protein comprising the SAG or its fragment or
XX CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
XX CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
XX CC exotoxin, Y. pseudotuberculosis SAG, Mycoplasma arthritides SAG and
XX CC Clostridium perfringens exotoxin. The method is useful in treating cancer
XX CC or malignant diseases such as malignant pleural effusion, ascites,
XX CC pericardial effusion or meningeal carcinomatosis. The present sequence
XX CC represents a Staphylococcal enterotoxin I (SEI) superantigen.
XX SQ Sequence 242 AA;
Query Match 27.4%; Score 339.5; DB 8; Length 242;
Best Local Similarity 35.6%; Pred. NO. 2e-25;
Matches 79; Conservative 36; Mismatches 74; Indels 33; Gaps 7;
QY 23 LSNLRQIY----YNEKAITENKESDDQFLENTLLFKGFTGHPWYNDLVLGSKDATN 78
DB 30 VGNLNFYTKHDYIDLKGVTDKNLPIANQLE-----PSTG---TNDLISESNWDEIS 79
QY 79 KYKGGKVDLYGAYGYQCAGGTPNKTACMYGVTLDHNNRLTEKKVPINLWIDGKQTTV 138
DB 80 KFKGKKLDIFGIDYNGPC-----KSKYMYGGATL--SGQYLNSARKIPINLWVNGHKHTI 132
QY 139 PIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFG--GK-----VQRGLIVF 186
DB 133 STDKIATNKKLVTAQEDIVKLRRLYQEEYNIYGHNTGKGYKSKFYSGFNCKVLV 192
QY 187 HSSEGSTVSYDLFDAGQGVPTDLLRIYRDNKNTINSENHIDL 228
DB 193 HLNNEKSFYVDLYFTYTGDLGVFLVSKYEDNKIIESEKPHLDV 234
RESULT 62
ADF89837
ID ADF89837 standard; protein; 240 AA.
XX AC ADF89837;
XX DT 26-FEB-2004 (first entry)
XX DE Staphylococcal enterotoxin L (SEL) superantigen.
XX KW Superantigen; SAG; Staphylococcal enterotoxin; SE; SEL; cytostatic;
XX KW gene therapy; cancer.

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RESULT 64
ID ADF89838 standard; protein; 239 AA.
XX ADF89838;
AC ADF89838;
DT 26-FEB-2004 (first entry)
DE Staphylococcal enterotoxin M (SEM) superantigen.
XX Superantigen; SAG; Staphylococcal enterotoxin; SE; SEM; cytostatic;
KW gene therapy; cancer.
XX Staphylococcus sp.
XX WO2003094846-A2.
XX 20-NOV-2003.
XX 08-MAY-2003; 2003WO-US014381.
XX 08-MAY-2002; 2002US-0378988P.
PR 15-JUN-2002; 2002US-0389366P.
PR 28-AUG-2002; 2002US-0406697P.
PR 29-AUG-2002; 2002US-0406750P.
PR 01-OCT-2002; 2002US-0415310P.
PR 02-OCT-2002; 2002US-0415400P.
PR 09-JAN-2003; 2003US-0438686P.
XX (TERM/) TERMAN D S.
PA Terman DS;
XX WPI; 2004-011997/01.
DR
XX
XX
PT Treating a subject with cancer or malignant diseases comprises
PT intratumoral, intrathecal or intracavitary administration of an amount of
PT a superantigen composition to the subject.
XX
XX
PS Disclosure; SEQ ID NO 15; 91pp; English.
XX
XX The invention relates to treating a subject with cancer. The method
CC involves administering an amount of a superantigen (SAG) composition
CC comprising a molecule selected from: a native SAG protein; its
CC biologically active fragment or a biologically active homologue or a
CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
CC exotoxin, Y. pseudotuberculosis SAG, Mycoplasma arthritides SAG and
CC Clostridium perfringens exotoxin. The method is useful in treating cancer
CC or malignant diseases such as malignant pleural effusion, ascites,
CC pericardial effusion or meningeal carcinomatosis. The present sequence
CC represents a Staphylococcal enterotoxin M (SEM) superantigen.
XX
XX Sequence 239 AA;
Query Match 25.8%; Score 320; DB 8; Length 239;
Best Local Similarity 33.0%; Pred. No. 1.8e-23;
Matches 72; Conservative 40; Mismatches 78; Indels 28; Gaps 6;
QY 25 NLROIYYNEKATENK--ESDDQFLENTLLFKGFFTGHPWYNLDLVLGSKDATNKYKG 82
DB 28 NLRN--YGSYPTEDHQSNPENNHLHQVLVS-----MDNSTVTAEKQVDDVKFKN 79
QY 83 KKVDLYGAYGYOCAGTGNKTCMYGVTLHNNRLTEKKVPINLWIDGKQTTVPIDK 142
DB 80 HAVDVYGLSYGYCL-----KNKYIYGVVTL-AGDYLKSRRIPINLWNGEHTQITSDK 133
QY 143 VKTSKEVTQVQLQARVHLHKGFGLY-----NSDSFGKQVQGLIVFHSSE 190
DB 134 VSTNKKLVTAQETDITKLRLYLOBEYNIYGFNDTNKGRNYGNKSKFSGGFNAGKILPHLND 193

QY 191 GSTVSYDLFDAQGGQYPTLLRIYRDNKTINSNLHIDL 228
DB 194 GSSFSYDLFDGTGTQQAESFLKIYNDNKTETEKFLDV 231

RESULT 65
ID ADF89832 standard; protein; 242 AA.
XX ADF89832;
AC ADF89832;
DT 26-FEB-2004 (first entry)
DE Staphylococcal enterotoxin G (SEG) superantigen.
XX Superantigen; SAG; Staphylococcal enterotoxin; SE; SEG; cytostatic;
KW gene therapy; cancer.
XX Staphylococcus sp.
XX WO2003094846-A2.
XX 20-NOV-2003.
XX 08-MAY-2003; 2003WO-US014381.
XX 08-MAY-2002; 2002US-0378988P.
PR 15-JUN-2002; 2002US-0389366P.
PR 28-AUG-2002; 2002US-0406697P.
PR 29-AUG-2002; 2002US-0406750P.
PR 01-OCT-2002; 2002US-0415310P.
PR 02-OCT-2002; 2002US-0415400P.
PR 09-JAN-2003; 2003US-0438686P.
XX (TERM/) TERMAN D S.
PA Terman DS;
XX WPI; 2004-011997/01.
DR
XX
XX
PT Treating a subject with cancer or malignant diseases comprises
PT intratumoral, intrathecal or intracavitary administration of an amount of
PT a superantigen composition to the subject.
XX
XX
PS Disclosure; SEQ ID NO 9; 91pp; English.
XX
XX The invention relates to treating a subject with cancer. The method
CC involves administering an amount of a superantigen (SAG) composition
CC comprising a molecule selected from: a native SAG protein; its
CC biologically active fragment or a biologically active homologue or a
CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
CC exotoxin, Y. pseudotuberculosis SAG, Mycoplasma arthritides SAG and
CC Clostridium perfringens exotoxin. The method is useful in treating cancer
CC or malignant diseases such as malignant pleural effusion, ascites,
CC pericardial effusion or meningeal carcinomatosis. The present sequence
CC represents a Staphylococcal enterotoxin G (SEG) superantigen.
XX
XX Sequence 242 AA;
Query Match 25.8%; Score 319.5; DB 8; Length 242;
Best Local Similarity 33.8%; Pred. No. 2e-23;
Matches 76; Conservative 35; Mismatches 71; Indels 43; Gaps 8;

QY 25 NLROIY--YNEK--AITENKESDDQFLENTLLFKGFFTGHPWYNLDLVLGSKDATNKY 80
DB 32 NLRFNFYANQPEKQLQGVSSGNFSTSHOLE---YIDGKYTLYSQFH-----NEY 76
QY 81 KKGK-----KVDLYGAYGYOCAGTGNKTCMYGVTLHNNRLTEKKVPINLWIDGKQ 135
DB 77 EAKRLKDHVDIFGISYGLC-----NTKMYGGITLANQN-LDKPRNIPINLWNGKQ 129

QY 136 TTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYN-----SDSFGGKVQRGL 183
Db 130 NTISTDKVSTQKEVTAQEIIDLKRLQNEVNIYGNKTKKGQEGYKSKFNSFNKGK 189
QY 184 IVFHSSEGSTVSYDLFDQAQQVPTDLLRIYRDNKTINSENHLIDL 228
Db 190 ITFHLNNEPSFTYDLFTYTGQAESFLKIYNDNKTIDAENFHLDV 234

RESULT 66
ADF89836
ID ADF89836 standard; protein; 242 AA.
XX
AC ADF89836;
XX
DT 26-FEB-2004 (first entry)
XX
DE Staphylococcal enterotoxin K (SEK) superantigen.
XX
KW Superantigen; SAg; Staphylococcal enterotoxin; SE; SEK; cytostatic;
KW gene therapy; cancer.
XX
OS Staphylococcus sp.
XX
PN WO2003094846-A2.
XX
PD 20-NOV-2003.
XX
PF 08-MAY-2003; 2003WO-US014381.
PR 08-MAY-2002; 2002US-0378988P.
PR 15-JUN-2002; 2002US-0389366P.
PR 28-AUG-2002; 2002US-0406697P.
PR 29-AUG-2002; 2002US-0406750P.
PR 01-OCT-2002; 2002US-0415310P.
PR 02-OCT-2002; 2002US-0415400P.
PR 09-JAN-2003; 2003US-0438686P.
XX
PA (TERM/) TERMAN D S.
XX
XX Terman DS;
XX
DR WPI; 2004-011997/01.
XX
PT Treating a subject with cancer or malignant diseases comprises
PT intratumoral, intrathecal or intracavitary administration of an amount of
PT a superantigen composition to the subject.
XX
PS Disclosure; SEQ ID NO 13; 91pp; English.
XX
CC The invention relates to treating a subject with cancer. The method
CC involves administering an amount of a superantigen (SAG) composition
CC comprising a molecule selected from: a native SAG protein; its
CC biologically active fragment or a biologically active homologue or a
CC biologically active fusion protein comprising the SAG or its fragment or
CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
CC exotoxin, Y. pseudotuberculosis SAg, Mycoplasma arthritides SAg and
CC Clostridium perfringens exotoxin. The method is useful in treating cancer
CC or malignant diseases such as malignant pleural effusion, ascites,
CC pericardial effusion or meningeal carcinomatosis. The present sequence
CC represents a Staphylococcal enterotoxin K (SEK) superantigen.
SQ Sequence 242 AA;

Query Match 25.0%; Score 310; DB 8; Length 242;
Best Local Similarity 33.2%; Pred. NO. 1.8e-22;
Matches 74; Conservative 39; Mismatches 76; Indels 34; Gaps 9;
QY 23 LSNLRQIY-----YNEKAITENKESDDQFLENTLLFKGFFTGHPYNDLLVDLGSKDYN 78
Db 29 IDNLRNFYTKKDFNLKDVKN-----DTPIANQLQF-----SNESY-DLISESKDFNFKS 78

QY 79 KYGKKVDLYGAYCYOCAGCTPNKTACMYGVTLHDNNRLTEKKVPINLWIDGKQTTV 138
Db 79 NFKGKLDVFGISYNGQC-----NTKYIYGITA-TNEYLDKPRNIPINIWINGHXTI 131
QY 139 PIDKVKTSKEVTVOELDLQARHYLHGKFLY-----NSDSFGK-----VORGLVLF 186
Db 132 STNKVSTNKKFVTAQEIIDLKRLRYLQBEYNTYGHNGTKKGEGYGHKSKFYSGFNIGKVTTF 191
QY 187 HSSEGSTVSYDLF-DAQQQVPTDLLRIYRDNKTINSENHLIDL 228
Db 192 HLNNDTFSYDLFTYTGDDGLPKSLKIYEDNKTVSEKFLHDV 234

RESULT 67
ABU79069
ID ABU79069 standard; protein; 266 AA.
XX
AC ABU79069;
XX
DT 18-JUN-2003 (first entry)
XX
DE S. aureus SEB (staphylococcus enterotoxin B) protein.
XX
KW Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
KW gene therapy; mammalian cell receptor; tumour associated lipid; anergy;
KW T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
KW APC; antitumour.
XX
OS Staphylococcus aureus.
XX
PN US2002177551-A1.
XX
PD 28-NOV-2002.
XX
PF 30-MAY-2001; 2001US-00870759.
XX
PR 31-MAY-2000; 2000US-0208128P.
XX
PA (TERM/) TERMAN D S.
XX
XX Terman DS;
XX
DR WPI; 2003-361759/34.
XX
PS N-PSDB; ACA64695.
XX
PT A mammalian cell receptor, useful in the treatment of cancer by binding
PT to tumour associated lipids where the binding induces anergy or apoptosis
PT in T cells and antigen presenting cells.
XX
PS Disclosure; Page; 167pp; English.
XX
CC The invention relates to a mammalian cell receptor, useful in the
CC treatment of cancer, which binds to tumour associated lipids and induces
CC anergy or apoptosis in the T cells and antigen presenting cells (APCs).
CC Also included are a mammalian cell useful in the treatment of cancer
CC where the receptor which binds tumour associated lipids and induces
CC cellular inactivation or death is deleted or functionally deactivated,
CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
CC (by allowing tumour associated lipids to contact immunocytes in which
CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
CC deleted), a construct useful in the treatment of cancer comprising a
CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
CC useful in the treatment of cancer (where an adaptor protein which
CC inhibits T cell activation by tumour associated antigens is deleted or
CC functionally deactivated), a composition useful in the treatment of
CC cancer (comprising a lipid raft conjugated to a superantigen), producing
CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
CC allowing tumour associated lipids to contact immunocytes, in which
CC receptors for the lipids are inactivated or deleted to produce a
CC tumouricidal immunocyte population, and administering the tumouricidal
CC activated immunocytes to the host), producing (M3) a tumouricidal APC


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RESULT 69
ADF43290
ID ADF43290 standard; protein; 266 AA.
XX
AC ADF43290;
XX
DT 12-FEB-2004 (first entry)
XX
DE Staphylococcal enterotoxin B polypeptide seq id 10.
XX
KW receptor; lipid-based tumour associated antigen; cytostatic;
KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
KW infectious disease; Staphylococcal enterotoxin B; SEB; enterotoxin B.
XX
OS Staphylococcus.
XX
FN US2003157113-A1.
XX
PD 21-AUG-2003..
XX
PF 28-DEC-2000; 2000US-00751708.
XX
PR 28-DEC-1999; 99US-0173371P.
XX
PA (TERM/) Terman D S.
XX
PI Terman DS;
XX
XX WPI; 2003-787326/74.
XX
PT New receptor in a mammalian cell that inhibits regular activation by
PT receptors specific for lipid-based tumor associated antigens, useful for
PT treating a neoplastic disease or tumor, and infectious diseases.
XX
PS Example 3; SEQ ID NO 10; 151pp; English.
XX
CC The invention describes a receptor in a mammalian cell that inhibits
CC regular activation by receptors specific for lipid-based tumour
CC associated antigen. The receptor has cytostatic and antimicrobial
CC properties and is suitable for use in gene therapy. The receptors,
CC methods and compositions are useful for treating a neoplastic disease or
CC tumour (cancer), and infectious diseases. This is the amino acid sequence
CC of an enterotoxin superantigen polypeptide the DNA encoding which can be
CC transfected in to a cell alone or with DNA encoding a cell surface moiety
CC to generate antitumour immunity.
XX
SQ Sequence 266 AA;
Query Match 24.3%; Score 300.5; DB 7; Length 266;
Best Local Similarity 33.6%; Pred. No. 1.9e-21;
Matches 82; Conservative 47; Mismatches 96; Indels 19; Gaps 8;
Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYNKAITENKESDDQFLNTLLFKGFFTG 60
Db 27 AESQDPKPKDELHKSSKE-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTK 84
Qy 61 HPWYNDLLVLDGSKDATNKKYKKVDLYGAYGYQC-----AGGTNKTACMYGG 110
Db 85 LGNYDNRVRFKPKDLADKYDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRTCMYGG 144
Qy 111 VTLHNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTQVELDLOARHVLHGKFGLY 170
Db 145 VTEHNGQLDKYRSITRVFPEDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLY 202
Qy 171 NSDSFGGKQVQRGLIVFHSSEGSTVSYDLFDAQGYPD--TLLRIYRDNKTINSENHLIDL 228
Db 203 EFN--SPYENGYIKFIENENS-FWYDMMAPGDKFDQSKYLMVNDNKNVDSKDKIEV 259
Qy 229 YLYT 232
Db 260 YLTT 263
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RESULT 70
AAW06737
ID AAW06737 standard; protein; 255 AA.
XX
AC AAW06737;
XX
DT 08-MAR-1997 (first entry)
XX
DE Staphylococcus enterotoxin B.
XX
KW Enterotoxin B; superantigen; antigen; cytokine; chemokine; T cell;
KW lymphocyte; monocyte; natural killer cell; gene therapy; cancer; vaccine;
KW adjuvant.
XX
OS Staphylococcus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..15
FT /label= Sig_peptide
XX
PN WO9636366-A1.
XX
PD 21-NOV-1996.
XX
PF 20-MAY-1996; 96WO-US007432.
XX
PR 18-MAY-1995; 95US-00446918.
PR 29-DEC-1995; 95US-00580806.
XX
PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX
PI Dow SW, Elmslie RE, Potter TA;
XX
DR WPI; 1997-011857/01.
DR N-PSDB; AAT45698.
XX
XX Recombinant molecule encoding superantigen and opt. cytokine or
PT chemokine - controls activity of effector cells (T cells, monocytes,
PT natural killer cells), used for gene therapy of cancer.
XX
PS Example 1; Page 96-97; 131pp; English.
XX
CC A cDNA clone (AAT45698) codes for staphylococcal enterotoxin B (AAW06737)
CC superantigen. Nucleic acids encoding superantigens (see also AAW06738-
CC 39), esp. truncated forms of the superantigen lacking the leader peptide,
CC can be utilised in the gene therapy of cancer, infectious diseases and
CC immunological disorders. The nucleic acid, optionally in combination with
CC cytokine or chemokine nucleic acids, is delivered to an animal using e.g.
CC liposomes. It acts by controlling the activity of effector cells, such as
CC T-cells, macrophages, monocytes and/or natural killer cells. Localised
CC prodn. of an effective but non-toxic amount of encoded proteins allows
CC safe treatment of the animal
XX
SQ Sequence 255 AA;
Query Match 24.2%; Score 300; DB 2; Length 255;
Best Local Similarity 34.0%; Pred. No. 2e-21;
Matches 83; Conservative 46; Mismatches 97; Indels 18; Gaps 7;
Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYNKAITENKESDDQFLNTLLFKGFFTG 60
Db 15 SMESQDPKPKDELHKSSKFTGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTK 73
Qy 61 HPWYNDLLVLDGSKDATNKKYKKVDLYGAYGYQC-----AGGTNKTACMYGG 110
Db 74 LGNYDNRVRFKPKDLADKYDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRTCMYGG 133
Qy 111 VTLHNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTQVELDLOARHVLHGKFGLY 170
Db 134 VTEHNGQLDKYRSITRVFPEDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLY 191
Qy 171 NSDSFGGKQVQRGLIVFHSSEGSTVSYDLFDAQGYPD--TLLRIYRDNKTINSENHLIDL 228
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Db 192 EFNN--SPYETGYIKFIENENS-FWYDMMAPAGDKFDQSKYLMYNDNRKQVDSKDVKIEV 248
Qy 229 YLYT 232
Db 249 YLYT 252

RESULT 71
ADF89825 standard; protein; 238 AA.
XX ADF89825;
AC ADF89825;
XX 26-FEB-2004 (first entry)
XX Staphylococcal enterotoxin B (SEB) superantigen.
DE Superantigen; SAg; Staphylococcal enterotoxin; SE; SEB; cytostatic;
KW gene therapy; cancer.
XX Staphylococcus sp.
OS Staphylococcus sp.
XX WO2003094846-A2.
XX 20-NOV-2003.
XX 08-MAY-2003; 2003WO-US014381.
XX 08-MAY-2002; 2002US-0378988P.
PR 15-JUN-2002; 2002US-0389366P.
PR 28-AUG-2002; 2002US-0406697P.
PR 29-AUG-2002; 2002US-0406750P.
PR 01-OCT-2002; 2002US-0415310P.
PR 02-OCT-2002; 2002US-0415400P.
PR 09-JAN-2003; 2003US-0438686P.
XX (TERM/) Terman D S.
XX Terman DS;
XX WPI; 2004-011997/01.
XX Treating a subject with cancer or malignant diseases comprises
PT intratumoral, intrathecal or intracavitary administration of an amount of
PT a superantigen composition to the subject.
XX Disclosure; SEQ ID NO 2; 91pp; English.

PS The invention relates to treating a subject with cancer. The method
CC involves administering an amount of a superantigen (Sag) composition
CC comprising a molecule selected from: a native Sag protein; its
CC biologically active fragment or a biologically active homologue or a
CC biologically active fusion protein comprising the Sag or its fragment or
CC homologue fused to a fusion partner polypeptide or peptide. The Sag is
CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
CC exotoxin, Y. pseudotuberculosis Sag, Mycoplasma arthritidis Sag and
CC Clostridium perfringens exotoxin. The method is useful in treating cancer
CC or malignant diseases such as malignant pleural effusion, ascites,
CC pericardial effusion or meningeal carcinomatosis. The present sequence
CC represents a Staphylococcal enterotoxin B (SEB) superantigen.
XX Sequence 238 AA;
SQ

Query Match 24.2%; Score 299.5; DB 8; Length 238;
Best Local Similarity 33.7%; Pred. No. 2.1e-21;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;
Qy 2 EKSEINEKDLRKKSGLQNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFTGH 61
Db 1 ESQDPKPKDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
Qy 62 PWNLDLLVGLSGDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTACMYGGV 111

Db 59 GYDNVRVFEFNKDLADKYDKYVDVFGANTYYQCYFSSKNTNDINSHQTDKRTCMYGV 118
Qy 112 TLHNNRLTEEKVPINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYSITVRVPEDGK-NLLSFD-VQTNKKVTAQELDYLTRHYLVKNKLYE 176
Qy 172 SDSFGKQVORGLIVPHSSEGSTSVYDLFPAQGOYPD--TLRIYRDNKTINSENHIDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMAPAGDKFDQSKYLMYNDNRKQVDSKDVKIEV 233
Qy 230 LYT 232
Db 234 LYT 236

RESULT 72
AAW64647
ID AAW64647 standard; peptide; 239 AA.
XX AAW64647;
XX 23-OCT-1998 (first entry)
XX Synthetic SEB protein fragment.
DE Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
XX Synthetic.
OS Staphylococcus aureus.
XX WO9829444-A1.
XX 09-JUL-1998.
XX 30-DEC-1997; 97WO-IL000438.
XX 30-DEC-1996; 96IL-00119938.
XX (YISS) YISSUM RES & DEV CO.
XX Kaempfer R, Arad G;
XX WPI; 1998-388042/33.
XX New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s).
XX Example 8; Page 41; 68pp; English.

CC AAW64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or TNF-
CC beta genes. The peptides may be used to prepare therapeutics or vaccines
CC for the treatment of prophylaxis of toxin-mediated activation of T cells
CC and eliciting protective immunity against toxic shock induced by PETs.
CC They can also be used for the treatment of harmful effects (especially
CC food poisoning) and toxic shock caused by PET. Antiserum to the peptides
CC can also be used for alleviating toxic shock induced by PET
XX Sequence 239 AA;
SQ

Query Match 24.2%; Score 299.5; DB 2; Length 239;
Best Local Similarity 33.7%; Pred. No. 2.1e-21;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;
Qy 2 EKSEINEKDLRKKSGLQNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFTGH 61

Db 1 ESQDPKPKDELHKSSKF-TGLMENNKKVLYDDNHVSAL-NVKSIDQFLYFDLIYSIKOTKL 58
Qy 62 PWYNDLLVGLGSKDATNKYKGGKVDLYGAYCYQC-----AGTPTNKTCMYGGV 111
Db 59 GNYDNVRVEFNKDLADKYDKYVDVFGANYYYCYFSSKKTNDINSHETDKRKTCTMYGGV 118
Qy 112 TLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLYE 176
Qy 172 SDSFGGKVQORGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRLIYRDNKNTINSENLIHDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMYNDNKNQVDSKDVKIEVY 233
Qy 230 LYT 232
Db 234 LTT 236

RESULT 73
AAB67341
ID AAB67341 standard; peptide; 239 AA.
XX AC AAB67341;
XX DT 23-APR-2001 (first entry)
XX DE Staphylococcus aureus enterotoxin B protein.
XX KW Tumour; cancer; immune; enterotoxin.
XX OS Staphylococcus aureus.
XX PN US6180097-B1.
XX PD 30-JAN-2001.
XX PF 30-OCT-1998; 98US-00183437.
XX PR 03-OCT-1989; 89US-00416530.
XX PR 17-JAN-1990; 90US-00466577.
XX PR 17-JAN-1991; 91WO-US000342.
XX PR 01-JUN-1992; 92US-00891718.
XX PR 02-MAR-1993; 93US-00025144.
XX PR 31-JAN-1994; 94US-00189424.
XX PR 19-JUN-1995; 95US-00491746.
XX PA (TERM/) TERMAN D S.
XX PI Terman DS;
XX DR WPI; 2001-158657/16.
XX PT Tumor cell capable of stimulating antitumor immune reactivity in vitro or
PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
PT costimulatory molecule.
XX PS Disclosure; Fig 2; 16pp; English.
XX CC The present invention relates to a tumour cell capable of stimulating
CC antitumor immune reactivity in vitro or in vivo contains and expresses an
CC exogenous nucleic acid molecule encoding a superantigen or its active
CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
CC molecule that activates T cells in conjunction with an antigenic
CC stimulus. The invention may be used for cancer therapy by stimulating an
CC anticancer immune response in vivo or ex vivo
XX Sequence 239 AA;

Query Match 24.2%; Score 299.5; DB 4; Length 239;
Best Local Similarity 33.7%; Pred. No. 2.1e-21;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;

Qy 2 EKSEINEKDLRKKSQELQNALSNLRQIYYTNEKAITENKESDDQFLENTLLFKGFFTGH 61
Db 1 ESQDPKPKDELHKSSKF-TGLMENNKKVLYDDNHVSAL-NVKSIDQFLYFDLIYSIKOTKL 58
Qy 62 PWYNDLLVGLGSKDATNKYKGGKVDLYGAYCYQC-----AGTPTNKTCMYGGV 111
Db 59 GNYDNVRVEFNKDLADKYDKYVDVFGANYYYCYFSSKKTNDINSHQTDKRKTCTMYGGV 118
Qy 112 TLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLYE 176
Qy 172 SDSFGGKVQORGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRLIYRDNKNTINSENLIHDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMYNDNKNQVDSKDVKIEVY 233
Qy 230 LYT 232
Db 234 LTT 236

RESULT 74
ABG75016
ID ABG75016 standard; protein; 239 AA.
XX AC ABG75016;
XX DT 12-FEB-2004 (first entry)
XX DE Unidentified Staphylococcus aureus protein.
XX KW Enterotoxin B; SEB; immunomodulatory; IgE antibody; atopic eczema;
KW lupus erythematosus; Crohn's disease; multiple sclerosis; psoriasis;
KW rheumatoid arthritis; immunoglobulin E; dermatological; antiasthmatic;
KW antiallergic; ophthalmological; antipsoriatic; antifungal;
KW antiarthritic; neuroprotective; immunosuppressive; antiinflammatory;
KW vasotropic; antidiabetic; thyromimetic; antibacterial; gynaecological;
KW cytostatic.
XX OS Staphylococcus aureus.
XX PN WO2003068812-A2.
XX PD 21-AUG-2003.
XX PF 14-FEB-2003; 2003WO-EP001511.
XX PR 15-FEB-2002; 2002DE-01007734.
XX PR 04-SEP-2002; 2002DE-01040866.
XX PA (AGEL-) AGELAB PHARMA GMBH.
XX PI Neuber K;
XX DR WPI; 2003-646480/61.
XX PT New polypeptide that binds immunoglobulin E and alters cytokine
PT synthesis, useful for treating e.g. atopic eczema, asthma or allergy,
PT also its encoding nucleic acid.
XX PS Disclosure; Page 45-46; 46pp; German.
XX CC The present invention relates to novel peptides derived from
CC Staphylococcus aureus enterotoxin B (SEB) protein. These peptides are
CC capable of binding to immunoglobulin (Ig) E antibodies. However, unlike
CC SEB, they do not induce proliferation of T cells. The peptides are useful
CC as immunomodulators and inhibitors of cytokine production in T cells,
CC particularly for treatment of atopic eczema, bronchial asthma, allergic
CC rhinoconjunctivitis, psoriasis, rheumatoid arthritis and multiple
CC sclerosis and for inducing or strengthening the Th1/Th2 immune responses,
CC specifically for treating psoriasis, autoimmune uveitis, allergic contact
CC eczema, Behcet's syndrome, diabetes mellitus, Hashimoto's thyroiditis,

CC infection by Helicobacter pylori, lupus erythematosus, Crohn's disease,
CC multiple sclerosis, organ transplant rejection, rheumatoid arthritis and
CC spontaneous, recurrent abortion. They can also be used, in vitro, for
CC inhibiting IFNgamma production and for modulating spontaneous or
CC stimulated cytokine production in Th1/Th2 cells. Note: No further
CC information about this sequence is given in the specification
XX
SQ Sequence 239 AA;

Query Match 24.2%; Score 299.5; DB 7; Length 239;
Best Local Similarity 33.7%; Pred. No. 2.1e-21;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;
QY 2 EKSEINEKDLRKSELRNALSRLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGH 61
DB 1 ESQDPKPELHKSKEF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWYNDLLVDSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGGV 111
DB 59 GNYDNVRVEFKNDLADKYKDYVDVFGANYYYQCYFSKKTNDINSHQDKRKTCHYGGV 118
QY 112 TLHDNNRLTEEEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYN 171
DB 119 TEHNGNQLDKYSITVRVFEDEK-NLLSFD-VQTNKKKVTAGELDLTRHYLVKNKKLYE 176
QY 172 SDSFGKVGQRLIVFHSSEGSTSVSYDLFDAQGYPD--TLRIYRDNKTINSENLHIDLY 229
DB 177 FNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDKNMVDKVKIEVY 233
QY 230 LYT 232
DB 234 LTT 236

RESULT 75
ADL14247
ID ADL14247 standard; protein; 239 AA.
AC ADL14247;
XX
DT 20-MAY-2004 (first entry)
DE Wild type Staphylococcus aureus enterotoxin B protein.
DE
KW staphylococcal enterotoxin B; SEB; immunogenicity;
KW T-cell peptide epitope; immune response.
XX
OS Staphylococcus aureus.
XX WO2004018684-A2.
XX
PD 04-MAR-2004.
XX
PP 18-AUG-2003; 2003WO-EP009116.
XX
PR 21-AUG-2002; 2002EP-00018229.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Carr FJ, Baker M, Carter G;
XX WPI; 2004-226855/21.
DR

XX New modified molecule having the biological activity of staphylococcal
XX enterotoxin B (SEB), useful as determinants on SEB able to evoke an
XX immune response.
XX
XX Disclosure; Page 4; 38pp; English.
XX
XX This invention relates to novel modified proteins that exhibit the
XX biological activity of Staphylococcal enterotoxin B (SEB) with reduced
XX immunogenicity compared to wild type proteins having the same biological
XX activity. Specifically, it refers to the identification of T-cell peptide

CC epitopes derived from SEB that can be modified in order to create
CC variants that are non-immunogenic. The present invention describes
CC designing SEB analogues containing amino acid substitutions in the most
CC immunogenic regions. Accordingly, the resulting modified molecules are
CC useful as determinants on SEB able to evoke an immune response. This
CC polypeptide sequence is the Staphylococcus aureus enterotoxin B protein
CC of the invention.
XX
SQ Sequence 239 AA;

Query Match 24.2%; Score 299.5; DB 8; Length 239;
Best Local Similarity 33.7%; Pred. No. 2.1e-21;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;
QY 2 EKSEINEKDLRKSELRNALSRLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGH 61
DB 1 ESQDPKPELHKSKEF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWYNDLLVDSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGGV 111
DB 59 GNYDNVRVEFKNDLADKYKDYVDVFGANYYYQCYFSKKTNDINSHQDKRKTCHYGGV 118
QY 112 TLHDNNRLTEEEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYN 171
DB 119 TEHNGNQLDKYSITVRVFEDEK-NLLSFD-VQTNKKKVTAGELDLTRHYLVKNKKLYE 176
QY 172 SDSFGKVGQRLIVFHSSEGSTSVSYDLFDAQGYPD--TLRIYRDNKTINSENLHIDLY 229
DB 177 FNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDKNMVDKVKIEVY 233
QY 230 LYT 232
DB 234 LTT 236

RESULT 76
AAW12153
ID AAW12153 standard; protein; 251 AA.
AC AAW12153;
XX
DT 04-NOV-1997 (first entry)
DE Streptococcus pyogenes Streptococcal toxin A mutant Cys908er.
DE
KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
KW protection; treatment; cancer; neutralising antibody;
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
KW hypotension; group A streptococcal infection; myositis; fascitis;
KW liver damage; T cell; lymphoma; ovarian; uterine.
XX
OS Streptococcus pyogenes.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..30 /label= sig_peptide
FT Peptide 31..251 /label= mat_peptide
FT Misc-difference 120 /note= "wild type Cys replaced by Ser"
FT
XX WO9640930-A1.
XX
PD 19-DEC-1996.
XX
PP 07-JUN-1996; 96WO-US010252.
XX
PR 07-JUN-1995; 95US-00480261.
XX
XX (MINU) UNIV MINNESOTA.
XX Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;

```

XX DR WPI; 1997-099936/09.
XX
XX PT Mutant SPE-A toxin with at least one amino acid change is substantially
XX PT non-lethal - used in vaccine composition for treatment of cancer and
XX PT streptococcal toxic shock syndrome etc.
XX
XX PS Example 4; Page; 102pp; English.
XX
XX CC The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
XX CC toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
XX CC animals against wild type SPE-A and to treat cancer and streptococcal
XX CC toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
XX CC antibodies (Ab) to be produced, which may be used to ameliorate STSS
XX CC symptoms, e.g. fever, hypotension, group A streptococcal infection,
XX CC myositis, fascitis and liver damage. The neutralising Ab is preferably
XX CC administered in conjunction with antibiotic therapy. The mutant SPE-A is
XX CC especially useful for treating T cell lymphomas, and ovarian and uterine
XX CC cancer. It is thought that mutant SPE-A can be selectively toxic to T
XX CC cell lymphoma cells. N.B. Sequence not given in the specification, but
XX CC constructed using the wild type SPE-A sequence given on pages 77-79
XX
XX SQ Sequence 251 AA;

Query Match      24.0%; Score 297.5; DB 2; Length 251;
Best Local Similarity 34.2%; Pred. No. 3.5e-21;
Matches 81; Conservative 45; Mismatches 92; Indels 19; Gaps 10;

Qy 4 SEENEKDLRKSELRNAL-SNLKQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFTG 60
Db 25 SQEFAQQDPDPQSLSRLSKVNLQNIYFLYEGDPVTHENVKSVQDLSSHLLIYN---VS 81
Qy 61 HPWYNDLLVLDLGSKDATNKYKGVKVDLYGAYGYOC-AGGTPNKTACMYGGVTLLHNNRL 119
Db 82 GPNYDKLTELKNEGMATFLKDKQNDIYGVYHLYCLYSENAERSACIYGGVTNHEGNHL 141
Qy 120 TEKKVPINLWDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGGKV 179
Db 142 EIPKKIVVKVSDIGIQ-SLSFD-IETNKKMTAQELDKVKRYLTDNKLQLYTNGP--SKY 197
Qy 180 QRGVLIVHSSSGSTVSVDLFD-----AQQYQPTLLRIYRDNKTINSENHLHDLYLT 232
Db 198 ETGVYKIFPKNKESFPWFDPFPEPEPTQSKY----LMYKDNETLSDNTSQIEVLYLT 250

RESULT 77
ABU62455
ID ABU62455 standard; protein; 266 AA.
XX
XX AC ABU62455;
XX
XX DT 27-AUG-2003 (first entry)
XX
XX DE S. aureus periplasmic enterotoxin B mutant Y94A.
XX
XX KW SEB; staphylococcal enterotoxin B; mutein; mutant; vaccine;
XX KW superantigen toxin; MHC; superantigen-associated bacterial infection;
XX KW bacterial infection; antibacterial.
XX
XX OS Staphylococcus aureus.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..26
XX FT /label= signal_peptide
XX FT Protein 27..266
XX FT /label= Mature_SEB_mutant
XX FT Misc-difference 121
XX FT /note= "Wild-type Tyr substituted by Ala"
XX
XX PN US2003036644-A1.
XX
XX PD 20-FEB-2003.

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XX PF 26-NOV-2001; 2001US-00002784.
XX
XX PR 25-JUN-1997; 97US-00882431.
XX PR 01-SEP-1998; 98US-00144776.
XX
XX PA (ULRI/) ULRICH R G.
XX
XX PI Ulrich RG;
XX
XX DR WPI; 2003-492125/46.
XX
XX PT New superantigen toxin DNA fragment, useful for preparing a composition
XX PT for treating or preventing bacterial infection.
XX
XX PS Example 3; Page; 68pp; English.
XX
XX CC The invention relates to an isolated and purified superantigen toxin DNA
XX CC fragment is altered so that binding of the encoded altered toxin to
XX CC either the MHC class II or T cell antigen receptor is altered. Also
XX CC included are a recombinant DNA construct (comprising a vector and an
XX CC isolated and purified altered superantigen toxin DNA fragment), a host
XX CC cell transformed with the recombinant DNA construct, producing altered
XX CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
XX CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
XX CC infection, a vaccine (comprising an altered superantigen toxin for
XX CC producing antigenic and immunogenic response resulting in the protection
XX CC of a mammal against superantigen-associated bacterial infection),
XX CC treating/ameliorating a superantigen-associated bacterial infection, an
XX CC antisera isolated from individuals immunised with one or more altered
XX CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
XX CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
XX CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
XX CC SPEb). The superantigen toxin DNA fragment is useful for preparing a
XX CC composition for treating or preventing bacterial infection. The present
XX CC sequence represents the Y94A (with reference to the mature protein
XX CC sequence) mutant of SEB. Note: The present sequence is not shown in the
XX CC specification but was created by the indexer using the wild-type sequence
XX CC and the information in the specification
XX
XX SQ Sequence 266 AA;

Query Match      24.0%; Score 297.5; DB 7; Length 266;
Best Local Similarity 33.2%; Pred. No. 3.8e-21;
Matches 81; Conservative 44; Mismatches 100; Indels 19; Gaps 7;

Qy 1 SEKSEENEKDLRKSELRNALSNLQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
Db 27 AESQDPKPDELHKSKF--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFLIYSIKDTK 84
Qy 61 HPWYNDLLVLDLGSKDATNKYKGVKVDLYGAYGYOCAGG-----TPNKTACMYGG 110
Db 85 LGDYDNVRVFPKNDLADKYDKYDVFGANYYYQCAFSEKKTNDINSHQTDKRTCMYGG 144
Qy 111 VTLHDNNRLTEKKVPINLWDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFLY 170
Db 145 VTEHNGQLDKYRSITVRVPEDGK-NLLSFD-VQTNKKKVTQAELDYLTRHYLVKNKKLY 202
Qy 171 NSDSFGGKQVQGLIVFHSSEGSTVSVDLFDAGQG--VPDITLLRIYRDNKTINSENHL 228
Db 203 EFN--SPYETGYIKFIENENS-FWYDMMPAGDFKFAQSKYLMYNDNMVDSKDVKIEV 259
Qy 229 YLYT 232
Db 260 YLTT 263

RESULT 78
AAR13209
ID AAR13209 standard; protein; 221 AA.
XX
XX AC AAR13209;
XX

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XX 03-OCT-1989; 89US-00416530.
PR 17-JAN-1990; 90US-00466577.
PR 17-JAN-1991; 91WO-US000342.
PR 01-JUN-1992; 92US-008931718.
PR 02-MAR-1993; 93US-00025144.
PR 31-JAN-1994; 94US-00189424.
PR 19-JUN-1995; 95US-00491746.
XX (TERM/) Terman D S.
XX Terman DS;
XX WPI; 2002-415198/44.
XX Reagent for treating cancer without the need for e.g. radiotherapy,
PT comprises a specific V beta subset of T cells sensitized to a growing
PT tumor and stimulated with superantigens.
XX Disclosure; Fig 2; 17pp; English.
XX The present sequence is the protein sequence of exotoxin A (SPE A) of
CC Streptococcus pyogenes. Similarity is shown, in several stretches of
CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
CC exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the
CC present invention, synthetic polypeptides useful in tumour therapy and in
CC blocking or destroying autoreactive T and B lymphocyte populations are
CC characterised by subantigenic structural homology to staphylococcal
CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
CC exotoxins, with statistically significant sequence homology and
CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
CC analysis exceeding 6) to include alignment of cysteine residues and
CC similar hydrophobic profiles. These superantigens are used to treat solid
CC tumours, including their metastases, without radiation, surgery or
CC standard chemotherapeutic agents. A claimed method of human cancer
CC treatment involves contacting haematopoietic cells from a patient with
CC one or more superantigens ex vivo to generate stimulated cells, selecting
CC a specific V beta subset of cells, and reintroducing these cells into the
CC patient to induce an in vivo therapeutic, tumouricidal reaction
XX Sequence 221 AA;
Query Match 23.9%; Score 296.5; DB 5; Length 221;
Best Local Similarity 35.6%; Pred. No. 3.7e-21;
Matches 80; Conservative 42; Mismatches 84; Indels 19; Gaps 10;
QY 16 SELQNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFTGHPWYNLLVDLG 72
DB 7 SQRHSSLVKLNQNIYFLYEGDPVTHENVKSVQDQLSHDLIYN---VSGPNYDKLTKELK 63
QY 73 SKDATNKYKGVLDLYGAYGYQC-AGGTPNKTACMYGGVTLHDNNRLTEKKYPINLWI 131
DB 64 NOEWATLFDKNVDIYGVYHLYCLENARSACIYGGVTHNHNHLEIIPKIVKRSI 123
QY 132 DGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQRLVIFHSSEG 191
DB 124 DGIQ-SLSFD-IETNKKWVAQELDYKVKYLTDNKQLYTNGP--SKYETGVKIFIPQNK 179
QY 192 STVSYDLFD---AQGYPTDLLRIYRDNKTINSENHLIDLYLT 232
DB 180 ESFWFDLPPEFTQSKY---LMIYKDNETLDSNTSQIEVLYLT 220
RESULT 81
AAW12151
ID AAW12151 standard; protein; 251 AA.
XX AC AAW12151;
XX 04-NOV-1997 (first entry)
XX Streptococcus pyogenes Streptococcal toxin A mutant Cys87Ser.
XX

KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
KW protection; treatment; cancer; neutralising antibody;
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
KW hypotension; group A streptococcal infection; myositis; fasciitis;
XX liver damage; T cell; lymphoma; ovarian; uterine.
OS Streptococcus pyogenes.
OS Synthetic.
XX Key Location/Qualifiers
FT Peptide 1..30
FT Peptide /label= sig_peptide
FT Peptide 31..251
FT Peptide /label= mat_peptide
FT Misc-difference 117
FT /note= "wild type Cys replaced by Ser"
XX WO9640930-A1.
XX 19-DEC-1996.
XX 07-JUN-1996; 96WO-US010252.
XX 07-JUN-1995; 95US-00480261.
XX (MINU) UNIV MINNESOTA.
PI Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
XX WPI; 1997-099936/09.
XX Mutant SPE-A toxin with at least one amino acid change is substantially
XX non-lethal - used in vaccine composition for treatment of cancer and
XX streptococcal toxic shock syndrome etc.
XX Example 4; Page; 102pp; English.
XX The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
XX toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
XX animals against wild type SPE-A and to treat cancer and streptococcal
XX toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
XX antibodies (Ab) to be produced, which may be used to ameliorate STSS
XX symptoms, e.g. fever, hypotension, group A streptococcal infection,
XX myositis, fasciitis and liver damage. The neutralising Ab is preferably
XX administered in conjunction with antibiotic therapy. The mutant SPE-A is
XX especially useful for treating T cell lymphomas, and ovarian and uterine
XX cancer. It is thought that mutant SPE-A can be selectively toxic to T
XX cell lymphoma cells. N.B. Sequence not given in the specification, but
XX constructed using the wild type SPE-A sequence given on pages 77-79
XX Sequence 251 AA;
Query Match 23.9%; Score 296.5; DB 2; Length 251;
Best Local Similarity 34.3%; Pred. No. 4.4e-21;
Matches 82; Conservative 44; Mismatches 90; Indels 23; Gaps 11;
QY 4 SEENEXDLRCKSLQNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFTG 60
DB 25 SQEYFAQDDPDSQQLHRSSLVKLNQNIYFLYEGDPVTHENVKSVQDQLSHHLIYN---VS 81
QY 61 HPWYNLLVDLGSDATNKYKGVLDLYGAYY---GYQCAGGTPNKTACMYGGVTLHDNN 117
DB 82 GPNYDKLTKELKNQEMATLFDKNVDIYGVYHLYCLENARSACIYGGVTHNHN 139
QY 118 RLTEKKYPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGG 177
DB 140 HLEIPKIVKVSIDGIQ-SLSFD-IETNKKWVAQELDYKVKYLTDNKQLYTNGP--S 195
QY 178 KVQGLVIFHSSEGSTVSYDLFD---AQGYPTDLLRIYRDNKTINSENHLIDLYLT 232
DB 196 KYETGYIKFIPKNKESFWFDLPPEFTQSKY---LMIYKDNETLDSNTSQIEVLYLT 250

QY	120	TEEKVPIINLWDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKGLVNSDSFGSKV	179
DB	142	EIPKIVVKSIDGIQ-SLSFD-IETNKKMVTAGELDYKVRKYLTDNKQLYINGP--SKY	197
QY	180	QRGLIVFHSSEGSTVSYLFD---AQQYPTDILLRIYRDNKTINSENHLIDLYLT	232
DB	198	ETGYIKFIPKONKESFWDFPEPEPTQSKY---LMIYKONETLDSNTSQIEVLVLT	250
<p>RESULT 83</p> <p>ADP89839</p> <p>ID ADP89839 standard; protein; 251 AA.</p> <p>AC ADP89839;</p> <p>XX</p> <p>XX 26-FEB-2004 (first entry)</p> <p>XX Streptococcal pyrogenic exotoxin A (SpEA) sequence.</p> <p>XX Superantigen; SAg; enterotoxin; cytostatic; gene therapy; cancer;</p> <p>KW pyrogenic exotoxin; SpE; SpEA.</p> <p>XX Streptococcus pyogenes.</p> <p>XX WO2003094846-A2.</p> <p>XX 20-NOV-2003.</p> <p>XX 08-MAY-2003; 2003WO-US014381.</p> <p>XX 08-MAY-2002; 2002US-0378988P.</p> <p>PR 15-JUN-2002; 2002US-0389366P.</p> <p>PR 28-AUG-2002; 2002US-0406697P.</p> <p>PR 29-AUG-2002; 2002US-0406750P.</p> <p>PR 01-OCT-2002; 2002US-0415310P.</p> <p>PR 02-OCT-2002; 2002US-0415400P.</p> <p>PR 09-JAN-2003; 2003US-0438686P.</p> <p>XX (TERM/) TERMAN D S.</p> <p>XX Terman DS;</p> <p>XX WPI; 2004-011997/01.</p> <p>XX</p> <p>XX Treating a subject with cancer or malignant diseases comprises</p> <p>PT intratumoral, intrathecal or intracavitary administration of an amount of</p> <p>PT a superantigen composition to the subject.</p> <p>XX</p> <p>XX Disclosure; SEQ ID NO 16; 91pp; English.</p> <p>XX</p> <p>XX The invention relates to treating a subject with cancer. The method</p> <p>CC involves administering an amount of a superantigen (SAG) composition</p> <p>CC comprising a molecule selected from: a native SAG protein; its</p> <p>CC biologically active fragment or a biologically active homologue or a</p> <p>CC biologically active fusion protein comprising the SAG or its fragment or</p> <p>CC homologue fused to a fusion partner polypeptide or peptide. The SAG is</p> <p>CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic</p> <p>CC exotoxin, Y. pseudotuberculosis SAg, Mycoplasma arthritides SAG and</p> <p>CC Clostridium perfringens exotoxin. The method is useful in treating cancer</p> <p>CC or malignant diseases such as malignant pleural effusion, ascites,</p> <p>CC pericardial effusion or meningeal carcinomatosis. The present sequence</p> <p>CC represents a Streptococcal pyrogenic exotoxin A (SpEA).</p> <p>XX</p> <p>XX Sequence 251 AA;</p>			
QY	4	SEBINEKDLRKKSELQNAL-SNLQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFTG	60
DB	25	SQVFAQQDDPQSLHRSSLVNQLNIYFLYEGDPVTHENVKSVQQLSHLLIYN---	81
QY	61	HPWYNLLVDLGSKDNTKYGKVDLYGAYGYQC-AGGTPTNKTACMYGGVTLHDNRRL	119
DB	82	GPNYDKLTKELKQEWATLFDKKNVDIYGVYVYHLYCYLCENASACIYGGVTNHEGNL	141

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QY 61 HPWYNDLLVLDGSKDATNKKYKGVLDLYGAYGYQC-AGGTPNKTACWYGVTLHDNNRL 119
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 82 GPNYDKLTELKQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGNHL 141
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 120 TEEKKVPINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV 179
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 142 EIPKKIVVKVSDIGIQ-SLSFD-IETNKKWMTAQELDYKVRKYLTDNKNQLYTNGP--SKY 197
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 180 QRGILVFHSSGSGTVSYDLFD----AQQYPTDLLRIYRDNKTINSENHLHDLYLT 232
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 198 ETGYIKFIPKNKESFWDFPEPEPTQSKY----LMIYKONETLDSNTSQIEVLYTT 250
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 84
AAW12154
ID AAW12154 standard; protein; 251 AA.
XX
AC AAW12154;
DT 04-NOV-1997 (first entry)
XX
DE Streptococcus pyogenes Streptococcal toxin A mutant Ser195Ala.
XX
KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
KW protection; treatment; cancer; neutralising antibody;
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
KW hypotension; group A streptococcal infection; myositis; fasciitis;
KW liver damage; T cell; lymphoma; ovarian; uterine.
XX
OS Streptococcus pyogenes.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT Peptide /label= sig_peptide
FT Peptide 31..251
FT Misc-difference 225 /label= mat_peptide
FT /note= "wild type Ser replaced by Ala"
XX
PN WO9640930-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US010252.
XX
PR 07-JUN-1995; 95US-00480261.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
XX
DR WPI; 1997-099936/09.
XX
PT Mutant SPE-A toxin with at least one amino acid change is substantially
PT non-lethal - used in vaccine composition for treatment of cancer and
PT streptococcal toxic shock syndrome etc.
XX
PS Example 4; Page; 102pp; English.
XX
CC The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
CC toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
CC animals against wild type SPE-A and to treat cancer and streptococcal
CC toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
CC antibodies (Ab) to be produced, which may be used to ameliorate STSS
CC symptoms, e.g. fever, hypotension, group A streptococcal infection,
CC myositis, fasciitis and liver damage. The neutralising Ab is preferably
CC administered in conjunction with antibiotic therapy. The mutant SPE-A is
CC especially useful for treating T cell lymphomas, and ovarian and uterine
CC cancer. It is thought that mutant SPE-A can be selectively toxic to T
CC cell lymphoma cells. N.B. Sequence not given in the specification, but
CC constructed using the wild type SPE-A sequence given on pages 77-79
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XX
SQ Sequence 251 AA;
Query Match 23.8%; Score 294.5; DB 2; Length 251;
Best Local Similarity 34.2%; Pred. No. 7.1e-21;
Matches 81; Conservative 45; Mismatches 92; Indels 19; Gaps 10;
QY 4 SEEINEKDLRKKSELORNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGPFPTG 60
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 25 SQEFAQODPDPQSQRHSSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHHLYN---VS 81
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 61 HPWYNDLLVLDGSKDATNKKYKGVLDLYGAYGYQC-AGGTPNKTACWYGVTLHDNNRL 119
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 82 GPNYDKLTELKQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGNHL 141
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 120 TEEKKVPINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV 179
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 142 EIPKKIVVKVSDIGIQ-SLSFD-IETNKKWMTAQELDYKVRKYLTDNKNQLYTNGP--SKY 197
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 180 QRGILVFHSSGSGTVSYDLFD----AQQYPTDLLRIYRDNKTINSENHLHDLYLT 232
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 198 ETGYIKFIPKNKESFWDFPEPEPTQAKY----LMIYKONETLDSNTSQIEVLYTT 250
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 85
AAW12146
ID AAW12146 standard; protein; 251 AA.
XX
AC AAW12146;
DT 04-NOV-1997 (first entry)
XX
DE Streptococcus pyogenes Streptococcal toxin A mutant Lys157Glu.
XX
KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
KW protection; treatment; cancer; neutralising antibody;
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
KW hypotension; group A streptococcal infection; myositis; fasciitis;
KW liver damage; T cell; lymphoma; ovarian; uterine.
XX
OS Streptococcus pyogenes.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT Peptide /label= sig_peptide
FT Peptide 31..251
FT Misc-difference 187 /label= mat_peptide
FT /note= "wild type Lys replaced by Glu"
XX
PN WO9640930-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US010252.
XX
PR 07-JUN-1995; 95US-00480261.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
XX
DR WPI; 1997-099936/09.
XX
PT Mutant SPE-A toxin with at least one amino acid change is substantially
PT non-lethal - used in vaccine composition for treatment of cancer and
PT streptococcal toxic shock syndrome etc.
XX
PS Claim 5; Page; 102pp; English.
XX
CC The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
CC toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
```

CC animals against wild type SPE-A and to treat cancer and streptococcal
 CC toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
 CC antibodies (Ab) to be produced, which may be used to ameliorate STSS
 CC symptoms, e.g. fever, hypotension, group A streptococcal infection,
 CC myositis, fascitis and liver damage. The neutralising Ab is preferably
 CC administered in conjunction with antibiotic therapy. The mutant SPE-A is
 CC especially useful for treating T cell lymphomas, and ovarian and uterine
 CC cancer. It is thought that mutant SPE-A can be selectively toxic to T
 CC cell lymphoma cells. N.B. Sequence not given in the specification, but
 CC constructed using the wild type SPE-A sequence given on pages 77-79
 XX
 SQ Sequence 251 AA;

Query Match 23.8%; Score 294.5; DB 2; Length 251;
 Best Local Similarity 34.2%; Pred. No. 7.1e-21;
 Matches 81; Conservative 45; Mismatches 92; Indels 19; Gaps 10;
 QY 4 SBEINEKDLRKXSELQNAL-SNLRLQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
 DB 25 SQEVAQQDDPDSQLRSSLVKNLQNIYFLYEGDPVTENKSVQDQLSHLLIYN--VS 81
 QY 61 HPWYNDLLVDLGSKDATNKYKGVLDYGYGYQC-AGTPTNKTACMYGGVTLHDNNRL 119
 DB 82 GPNYDKLKTQLKNQEMATLFDKQNDVIYGVYHLYCLCENAEASACIYGGVTNHEGNHL 141
 QY 120 TEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTQVELDLQARHYLHGKFLYNSDSFGKV 179
 DB 142 EIPKIVKVSIDGIQ-SLSFD-IEINKKQVTAQLDYKVRKYLTDNEQLYNGP--SKY 197
 QY 180 QRLIVFHSSEGSTVSYDLFD----AQGYPTDTLRIYRDNKTINSENLHIDLTYLT 232
 DB 198 ETGYIKFIPKNKESFWDFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVLYLT 250
 RESULT 86
 AAW12097
 ID AAW12097 standard; protein; 251 AA.
 AC AAW12097;
 XX
 XX 04-NOV-1997 (first entry)
 DE Streptococcus pyogenes Streptococcal toxin A.
 KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
 KW protection; treatment; cancer; neutralising antibody;
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
 KW hypotension; group A streptococcal infection; myositis; fascitis;
 KW liver damage; T cell; lymphoma; ovarian; uterine.
 XX
 OS Streptococcus pyogenes.
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..30
 FT /label= sig_peptide
 FT Peptide 31..251
 FT /label= mat_peptide
 XX
 PN WO9640930-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US010252.
 XX
 PR 07-JUN-1995; 95US-00480261.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
 XX WPI; 1997-099936/09.
 DR N-PSDB; AAW12097.
 XX

PT Mutant SPE-A toxin with at least one amino acid change is substantially
 PT non-lethal - used in vaccine composition for treatment of cancer and
 PT streptococcal toxic shock syndrome etc.
 XX
 PS Disclosure; Page 77-79; 102pp; English.
 XX
 CC The present sequence is Streptococcus pyogenes Streptococcal toxin A (SPE
 CC -A), from which a non-lethal mutant SPE-A, comprising at least 1 amino
 CC acid change, can be derived. The mutant SPE-A can be used to produce
 CC vaccines to protect animals against wild type SPE-A and to treat cancer
 CC and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes
 CC neutralising antibodies (Ab) to be produced, which may be used to
 CC ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal
 CC infection, myositis, fascitis and liver damage. The neutralising Ab is
 CC preferably administered in conjunction with antibiotic therapy. The
 CC mutant SPE-A is especially useful for treating T cell lymphomas, and
 CC ovarian and uterine cancer. It is thought that mutant SPE-A can be
 CC selectively toxic to T cell lymphoma cells
 XX
 SQ Sequence 251 AA;

Query Match 23.8%; Score 294.5; DB 2; Length 251;
 Best Local Similarity 34.2%; Pred. No. 7.1e-21;
 Matches 81; Conservative 45; Mismatches 92; Indels 19; Gaps 10;
 QY 4 SBEINEKDLRKXSELQNAL-SNLRLQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
 DB 25 SQEVAQQDDPDSQLRSSLVKNLQNIYFLYEGDPVTENKSVQDQLSHLLIYN--VS 81
 QY 61 HPWYNDLLVDLGSKDATNKYKGVLDYGYGYQC-AGTPTNKTACMYGGVTLHDNNRL 119
 DB 82 GPNYDKLKTQLKNQEMATLFDKQNDVIYGVYHLYCLCENAEASACIYGGVTNHEGNHL 141
 QY 120 TEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTQVELDLQARHYLHGKFLYNSDSFGKV 179
 DB 142 EIPKIVKVSIDGIQ-SLSFD-IEINKKQVTAQLDYKVRKYLTDNEQLYNGP--SKY 197
 QY 180 QRLIVFHSSEGSTVSYDLFD----AQGYPTDTLRIYRDNKTINSENLHIDLTYLT 232
 DB 198 ETGYIKFIPKNKESFWDFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVLYLT 250
 RESULT 87
 AAW12147
 ID AAW12147 standard; protein; 251 AA.
 AC AAW12147;
 XX
 XX 04-NOV-1997 (first entry)
 DE Streptococcus pyogenes Streptococcal toxin A mutant Asn20Aep.
 KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
 KW protection; treatment; cancer; neutralising antibody;
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
 KW hypotension; group A streptococcal infection; myositis; fascitis;
 KW liver damage; T cell; lymphoma; ovarian; uterine.
 XX
 OS Streptococcus pyogenes.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..30
 FT /label= sig_peptide
 FT Peptide 31..251
 FT /label= mat_peptide
 FT Misc-difference 50
 FT /note= "wild type Asn replaced by Asp"
 XX
 PN WO9640930-A1.
 XX
 PD 19-DEC-1996.
 XX

XX SPE-A toxin; nonlethal; mutant; Streptococcus pyogenes exotoxin A;
 KW wild type; nontoxic; antibody; vaccine; immunity; ovarian cancer;
 KW streptococcal toxic shock syndrome; STSS; T cell lymphoma;
 KW uterine cancer.
 XX Streptococcus pyogenes.
 OS WO9824911-A2.
 XX
 PN 11-JUN-1998.
 XX
 PD 05-DEC-1997; 97WO-US022228.
 XX
 PF 06-DEC-1996; 96US-0032930P.
 XX
 PR (MINU) UNIV MINNESOTA.
 XX
 PA Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
 XX
 PI WPI; 1998-333330/29.
 XX
 DR N-PSDB; AAV41593.
 XX
 DN New mutant Streptococcal SPE-A toxins - useful for, e.g. prevention or
 XX treatment of streptococcal infection or toxic shock syndrome.
 PT
 PS Disclosure; Fig 3; 95pp; English.
 XX
 XX This is the amino acid sequence of the Streptococcus pyogenes exotoxin A
 CC (SPE-A toxin). The novel mutant Streptococcal SPE-A toxin has at least 1
 CC aa change and is nonlethal compared with a protein to wild type SPE-A
 CC toxin. The mutant SPE-A toxins are nontoxic and can produce antibodies
 CC that neutralise wild type SPE-A toxin activity. The toxins can be used in
 CC vaccines and therapeutics to generate a protective immune response
 CC against streptococcal infection. They can be used to protect against the
 CC development of streptococcal toxic shock syndrome (STSS). In addition,
 CC the toxins can be used for treating animals with symptoms of
 CC streptococcal infection or STSS and in methods for stimulating T cell
 CC proliferation and in the treatment of cancer. In particular they can be
 CC used for treating T cell lymphomas, and ovarian and uterine cancer.
 XX
 SQ Sequence 251 AA;
 Query Match 23.8%; Score 294.5; DB 2; Length 251;
 Best Local Similarity 34.2%; Pred. No. 7.1e-21;
 Matches 81; Conservative 45; Mismatches 92; Indels 19; Gaps 10;
 QY 4 SEEINEKDLRKSELRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFTG 60
 DB 25 SQEVPAAQDDPDSQLRSSLVKNLQNIYFLYEGDPVTHENVKSVDDQLLGHILYN---VS 81
 QY 61 HPWYNDLLVDLGSKDATNKYKGGVDLYGAYGYQC-AGGTPNKTAQMYGGVTLHDNNRL 119
 DB 82 GPNYDKLTKLNQEMATLFDKQNDVIYGVYHLCYLCENAEASACIYGGVTNHEGHL 141
 QY 120 TEEKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHLYLHGKFLYNSDSFGKV 179
 DB 142 EIPKLIWVKSIDIGQ-SLSFD-IETNKQVTAQLDYKVKYLTDNKQLYNGP--SKY 197
 QY 180 QRGLIVFHSSEGSTVSIDYLFDP-----AQGYPTDLLRIYRDNKTINSENLHIDLYLT 232
 DB 198 ETGYIKFIPKNKESFWDFPEPEFTQSKY----LMIYKDNELTDSNTSQIEVLYLT 250
 RESULT 90
 AAY06254
 ID AAY06254 standard; protein; 239 AA.
 XX
 AC AAY06254;
 XX
 XX 23-AUG-1999 (first entry)
 DT
 XX Staphylococcal group C enterotoxin SEC3-FRI909.
 DE

XX Enterotoxin; SEC3-FRI909; toxin; disulfide loop; protein engineering.
 KW Staphylococcus aureus.
 OS
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 93..110
 XX
 PN WO9927889-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 01-DEC-1998; 98WO-US025107.
 XX
 PR 02-DEC-1997; 97US-0067357P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Bohach GI;
 XX
 DR WPI; 1999-358008/30.
 XX
 DN Non-toxic modified staphylococcal enterotoxins.
 XX
 PT Disclosure; Page 17; 25pp; English.
 PS
 XX This protein represents the Staphylococcus aureus type C enterotoxin SEC3
 CC -FRI909. The invention relates to pyrogenic toxins, such as
 CC staphylococcal enterotoxins, modified in the disulfide loop region.
 CC Typically, the modification involves deletions within the disulfide loop
 CC region of SEC (see AAY06261). The modified toxins retain useful
 CC biological properties, such as the ability to induce cytokine production,
 CC but have substantially reduced toxicity compared to the corresponding
 CC unmodified native toxin. Emetic response inducing activity and fever
 CC inducing activity are typically decreased by at least about 100-fold,
 CC while LD50 (in Dutch Belted rabbits) is at least 100-fold higher than the
 CC native toxin
 XX
 SQ Sequence 239 AA;
 Query Match 23.7%; Score 293.5; DB 2; Length 239;
 Best Local Similarity 33.3%; Pred. No. 8.3e-21;
 Matches 78; Conservative 48; Mismatches 89; Indels 19; Gaps 9;
 QY 11 DLRKSELRNALSNLRQIYYNEKAITENK-ESDDQFLENTLLFKGFTGHPWYNDLV 69
 DB 10 DLHKSEEF-TGTWGNMK--LYDDHVVSATKVSVDKFLAHLIYNINDKLNNDKVKVT 66
 QY 70 DLGSKDATNKYKGGVDLYGAYGYQC-----AGGTENKTAQMYGGVTLHDNNRLTEE 122
 DB 67 ELLNEDLANKYKDEVVDVYVGSNYVNCYFSSKDNVGVKTSKGTCTMYGGITKIEGHNFDNG 126
 QY 123 --KKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHLYLHGKFLYNSDSFGKVQ 180
 DB 127 NQONVLLIRY-ENKRNITISFE-VQTDKSVTAQLDIKARNFLINKNLNLYEFNS--SPYE 182
 QY 181 RGLIVFHSSEGSTVSIDYLFDAQGYPD--TLRIYRDNKTINSENLHIDLYLT 232
 DB 183 TGYIKFIESNGTTFWYDMMPAFCDKFDQSKLMYIKDNKMWDSKSVKIEVHLTT 236
 RESULT 91
 ABG71370
 ID ABG71370 standard; protein; 240 AA.
 XX
 AC ABG71370;
 XX
 XX 29-JAN-2003 (first entry)
 DT
 XX Staphylococcal enterotoxin SEC3-FRI909.
 DE
 XX Modified pyrogenic toxin; disulfide loop; fever-inducing activity;
 KW emetic response-inducing activity; staphylococcal enterotoxin;
 DE

KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
 KW SEC3-FRI909.
 OS Staphylococcus aureus.
 XX Key Location/Qualifiers
 FH Misc-difference 240
 FT /label= unknown
 XX
 XX WO200283169-A1.
 XX 24-OCT-2002.
 XX
 XX 11-APR-2002; 2002WO-US011619.
 XX 13-APR-2001; 2001US-0283720P.
 XX (IDAH-) IDAHO RES FOUND INC.
 XX Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
 XX WPI; 2003-058608/05.
 XX
 XX New modified staphylococcal enterotoxin derived from a native disulfide
 PT loop-containing pyrogenic toxin, useful for non-specifically enhancing an
 PT immune function and as a vaccine against toxic shock syndrome or food
 PT poisoning.
 XX
 XX Disclosure; Fig 15; 67pp; English.
 XX
 XX The invention relates to a modified pyrogenic toxin derived from a native
 CC disulphide loop-containing pyrogenic toxin where the modified toxin
 CC comprises a disulphide loop having no more than 10 amino acids. The
 CC modified toxin has a fever-inducing activity or an emetic response-
 CC inducing activity decreased by about 100-fold in comparison to a native
 CC toxin. The modified pyrogenic toxin, that is a staphylococcal
 CC enterotoxin, is useful for non-specifically enhancing an immune function
 CC and for vaccination against diseases such as toxic shock syndrome and
 CC food poisoning. This sequence represents the staphylococcal enterotoxin,
 CC SEC3-FRI909
 XX
 XX Sequence 240 AA;
 SQ
 Query Match 23.7%; Score 293.5; DB 6; Length 240;
 Best Local Similarity 33.3%; Pred. No. 8.3e-21;
 Matches 78; Conservative 48; Mismatches 89; Indels 19; Gaps 9;
 Qy 11 DLKKSELQRLNALNRQIYYNNEKAITENK-ESDQDFLENTLLFKGFTTGHWPYNLLV 69
 Db 10 DLKSEEF-TGTWGNMK--LYDDHYVSATKVKSVDFLAHDLIYNINDKLNNDYDKVKT 66
 Qy 70 DLGSKDATNKYGGKVDLYGAYGYQC-----AGTPTNKATACMGVTLHDNRLTEE 122
 Db 67 ELNEDLANKYKDEVDVYGSNYVNCYFSSKDNVGVKTSKGTCTMYGKITKHEGNHFDNG 126
 Qy 123 --KVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHLYHGKFGLYNSDSFGGKVQ 180
 Db 127 NLQNVLRVY-ENKRTISFE-VQTDKASVTAQELDIKARFLNKKNLVFNFS--SPYE 182
 Qy 181 RGLIVFHSSEGSTVSYDLFDAQGGYD--TLLRIYRDNKNTINSENHLIDLYLT 232
 Db 183 TGYIKFIESNGTWFYDMMPPAGDKFDQSKYLMYKDKMVDKSVKIEVHLT 236
 RESULT 92
 ABB79503
 ID ABB79503 standard; protein; 266 AA.
 XX
 XX ABB79503;
 AC
 XX
 DT 23-SEP-2002 (first entry)
 XX
 XX DE Staphylococcal enterotoxin B vaccine (B42360210).

XX Enterotoxin B; superantigen; antigen; toxin; vaccine; B42360210;
 KW attenuation.
 XX Staphylococcus sp.
 XX US6399332-B1.
 XX 04-JUN-2002.
 XX
 XX 01-SEP-1998; 98US-00144776.
 XX 25-JUN-1997; 97US-00882431.
 XX (USSA) US SEC OF ARMY.
 XX Ulrich RG, Olson MA, Bavari S;
 XX WPI; 2002-546281/58.
 XX N-PSDB; ABN84224.
 XX
 XX Novel isolated and purified superantigen toxin DNA fragment which has
 PT been genetically altered, useful for producing vaccine for treatment of
 PT superantigen toxin-associated bacterial diseases.
 XX
 XX Disclosure; Col 41-43; 46pp; English.
 XX
 XX The present sequence is the protein sequence of staphylococcal
 CC enterotoxin B (SEB) vaccine B42360210. The invention relates to a vaccine
 CC against superantigen toxin-associated bacterial diseases. Superantigen
 CC vaccines were developed by engineering changes in the receptor-binding
 CC portions of superantigen toxins such as SEB to reduce receptor-binding
 CC affinities and toxicity while maintaining antigenicity. In examples from
 CC the invention, attenuated superantigen toxins were shown to protect
 CC animals against challenge with wild-type toxin. Methods of producing and
 CC using the altered superantigen toxins as vaccines, and in diagnosis and
 CC therapy, are provided. A multivalent vaccine consisting of altered
 CC superantigen toxins from SEA, SEB, SEC-1, TSST-1 and streptococcal SPEa
 CC is predicted to provide protective immunity against the majority of
 CC bacterial superantigen toxins
 XX
 XX Sequence 266 AA;
 SQ
 Query Match 23.7%; Score 293.5; DB 5; Length 266;
 Best Local Similarity 32.8%; Pred. No. 9.7e-21;
 Matches 80; Conservative 45; Mismatches 100; Indels 19; Gaps 7;
 Qy 1 SEKSEETNEKDLRKKSELQRLNALNRQIYYNNEKAITENKESDDQFLENTLLFKGFTT 60
 Db 27 AESQDPKPDDELHKSKF--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTK 84
 Qy 61 HPWYNDLLVDLGSKDATNKYGGKVDLYGAYGYQC-----AGTPTNKATACMYGG 110
 Db 85 LGDYDNRVRFKNDLADKDKYDVFVGANYYYQCYFSSKNTDINSHQTDKRTCTMYGG 144
 Qy 111 VTLDHNNRLTEKKVPTINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHLYHGKFGLY 170
 Db 145 VTEHNGQLDKYRITVRVFDGK-NLLSPD-VQTNKKVTAQELDYLTRYLVKNKKLY 202
 Qy 171 NSDSFGGKQVRLIVFHSSEGSTVSYDLFDAQGG--YPTLLRIYRDNKNTINSENHLIDL 228
 Db 203 EFNN--SPYETGYIKFTIENENS-FWYDMMPPAGDKFAQSKYLMYNDNMVDKDKIEV 259
 Qy 229 YLYT 232
 Db 260 YLTT 263
 RESULT 93
 ABU10083
 ID ABU10083 standard; protein; 266 AA.
 XX
 XX AC ABU10083;

XX 11-AUG-2003 (first entry)
XX Staphylococcal enterotoxin B #1.
XX Enterotoxin B; superantigen-associated bacterial infection; vaccine;
KW superantigen toxin.
XX Staphylococcus sp.
OS US2003009015-A1.
XX 09-JAN-2003.
XX 25-JUN-1997; 97US-00882431.
XX 25-JUN-1997; 97US-00882431.
XX (ULRI/) ULRICH R G.
PA (OLSO/) OLSON M A.
PA (BAVA/) BAVARI S.
PI Ulrich RG, Olson MA, Bavari S;
XX WPI; 2003-401542/38.
DR N-PSDB; ACA61179.
XX New superantigen toxin and/or DNA fragment with an altered binding of the
PT encoded altered toxin to either MHC class II or T cell antigen receptor,
PT useful for treating or ameliorating superantigen-associated bacterial
PT infection.
XX Claim 12; Page 23-24; 50pp; English.
XX The invention relates to an isolated and purified superantigen toxin
CC and/or DNA fragment, which has been altered so that the binding of the
CC encoded toxin to either major histocompatibility complex (MHC) class II
CC or T cell antigen receptor is altered. The superantigen toxins, DNA
CC fragments, and vaccines are useful for treating or ameliorating
CC superantigen-associated bacterial infection. The DNA fragments are
CC particularly useful for producing vaccine against superantigen toxin
CC infections. The transformed host cells are useful for analysing the
CC effectiveness of drugs and agents that affect the binding of
CC superantigens to MHC class II or T-cell antigen receptors. The present
CC sequence represents the amino acid sequence of staphylococcal enterotoxin
CC B #1
XX
SQ Sequence 266 AA;
Query Match 23.7%; Score 293.5; DB 6; Length 266;
Best Local Similarity 32.8%; Pred. No. 9.7e-21;
Matches 80; Conservative 45; Mismatches 100; Indels 19; Gaps 7;
QY 1 SEKSEINEKDLRKKSSELOLNLSNRQIYYNEKAITENKESDDOFLNTLFGFTG 60
DB 27 AESQDPKPKDELHKSFK--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSKDTK 84
QY 61 HPWYNDLLVGLSKDATNKYKGVLDYGYGYQC-----AGGTPNKTCMYGG 110
DB 85 LGDYDNVRVEFKNLADKYDVDFGANYYYQCYFSKKTINDINSHQDKRKTMYGG 144
QY 111 VTLHDNNRLTEEEKVPINLWDGKQTPVDKVKTSKKEVTVOELDQARHYLHGRFGLY 170
DB 145 VTEHNGQLDKYSITVRVEDGK-NLLSFD-VQTNKKKTAQELDYLTREHYLVKNKLY 202
QY 171 NSDSFGKVGQRLIVFHSSEGSTVSVDLDAQGQ--YPTDLLRIYRDNKNTINSENHLIDL 228
DB 203 EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFAQSKYLMWYNDKNMVDKDKVIEV 259
QY 229 YLYT 232
DB 260 YLTT 263

RESULT 94
ABU62326
ID ABU62326 standard; protein; 266 AA.
XX AC ABU62326;
XX 27-AUG-2003 (first entry)
XX S. aureus wild-type enterotoxin B, SEB.
XX SEB; staphylococcal enterotoxin B; vaccine; superantigen toxin; MHC;
KW superantigen-associated bacterial infection; bacterial infection;
KW antibacterial.
XX Staphylococcus aureus.
XX Key Location/Qualifiers
FT Peptide 1..27
FT Protein /label= Signal_peptide
FT /label= Mature_SEB
XX US2003036644-A1.
XX 20-FEB-2003.
XX 26-NOV-2001; 2001US-00002784.
XX 25-JUN-1997; 97US-00882431.
PR 01-SEP-1998; 98US-00144776.
XX (ULRI/) ULRICH R G.
XX Ulrich RG;
XX WPI; 2003-492125/46.
DR N-PSDB; ACD28896.
XX New superantigen toxin DNA fragment, useful for preparing a composition
PT for treating or preventing bacterial infection.
XX Disclosure; Page 26-27; 68pp; English.
XX The invention relates to an isolated and purified superantigen toxin DNA
CC fragment is altered so that binding of the encoded altered toxin to
CC either the MHC class II or T cell antigen receptor is altered. Also
CC included are a recombinant DNA construct (comprising a vector and an
CC isolated and purified altered superantigen toxin DNA fragment), a host
CC cell transformed with the recombinant DNA construct, producing altered
CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
CC infection, a vaccine (comprising an altered superantigen toxin for
CC producing antigenic and immunogenic response resulting in the protection
CC of a mammal against superantigen-associated bacterial infection),
CC treating/ameliorating a superantigen-associated bacterial infection, an
CC antiserum isolated from individuals immunised with one or more altered
CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
CC SEB, SECI) and streptococcal pyrogenic enterotoxin a and b (SPEa and
CC SEPB). The superantigen toxin DNA fragment is useful for preparing a
CC composition for treating or preventing bacterial infection. The present
CC sequence represents wild-type SEB
XX
SQ Sequence 266 AA;
Query Match 23.7%; Score 293.5; DB 7; Length 266;
Best Local Similarity 32.8%; Pred. No. 9.7e-21;
Matches 80; Conservative 45; Mismatches 100; Indels 19; Gaps 7;
QY 1 SEKSEINEKDLRKKSSELOLNLSNRQIYYNEKAITENKESDDOFLNTLFGFTG 60
DB 27 AESQDPKPKDELHKSFK--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSKDTK 84

Qy 61 HPWYNDLIVDLGSKDATNKYKGVLDLYGAYGYQC-----AGGTPNKTACMYGG 110
Db 85 LGDYDNVRVEFNKDLADKYKDYVDVFGANYYYQCYFSKKTNDINSHQTDKRTKCYMG 144
Qy 111 VTLDHNNRLTBEKKVPINLWIDGQTTVPIDKVKTSKEKVTQBELDQARHYLHGKFGLY 170
Db 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLY 202
Qy 171 NSDSFGGKQVQGLVHFHSSGEGSTVSYDLFDAQGO--YPTDILLRIYRDNKTINSENHLIDL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFAQSKYLLMMYNDNMVDSKDVKIEV 259
Qy 229 YLYT 232
Db 260 YLTT 263
RESULT 95
AAE37678
ID AAE37678 standard; protein; 266 AA.
XX AC AAE37678;
XX DT 06-OCT-2003 (first entry)
XX DE Protein #3 related to the invention.
XX KW Superantigen toxin; vaccine; infection; gene therapy.
XX OS Unidentified.
XX PN WO2003056015-A1.
XX PD 10-JUL-2003.
XX PF 26-NOV-2001; 2001WO-US046540.
XX PR 26-NOV-2001; 2001US-00002784.
XX FA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX PI Ulrich RG;
XX DR WPI; 2003-492125/46.
XX DR N-PSDB; AAD56766.
XX PT New superantigen toxin DNA fragment, useful for preparing a composition
XX PT for treating or preventing bacterial infection.
XX PS Disclosure; Page 114-115; 141pp; English.
XX CC The invention provides a superantigen toxin DNA fragment which has been
XX CC genetically altered such that binding of the encoded altered toxin to
XX CC either the MHC class II or T cell antigen receptor is disrupted or
XX CC altered. DNA fragments of the invention are useful in the production of
XX CC vaccines against bacterial superantigen toxin infections. They are also
XX CC useful in gene therapy. The present sequence is a protein related to the
XX CC invention
SQ Sequence 266 AA;
Query Match 23.7%; Score 293.5; DB 7; Length 266;
Best Local Similarity 32.8%; Pred. No. 9.7e-21;
Matches 80; Conservative 45; Mismatches 100; Indels 19; Gaps 7;
Qy 1 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFFTG 60
Db 27 AESQDPKPELHKSSKP--TCLMEDMKVLVDNHNVSAINVKSIDQFLYFDLIYSIKDTK 84
Qy 61 HPWYNDLIVDLGSKDATNKYKGVLDLYGAYGYQC-----AGGTPNKTACMYGG 110
Db 85 LGDYDNVRVEFNKDLADKYKDYVDVFGANYYYQCYFSKKTNDINSHQTDKRTKCYMG 144

Qy 111 VTLDHNNRLTBEKKVPINLWIDGQTTVPIDKVKTSKEKVTQBELDQARHYLHGKFGLY 170
Db 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLY 202
Qy 171 NSDSFGGKQVQGLVHFHSSGEGSTVSYDLFDAQGO--YPTDILLRIYRDNKTINSENHLIDL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFAQSKYLLMMYNDNMVDSKDVKIEV 259
Qy 229 YLYT 232
Db 260 YLTT 263
RESULT 96
AAB67344
ID AAB67344 standard; peptide; 221 AA.
XX AC AAB67344;
XX DT 23-APR-2001 (first entry)
XX DE Streptococcus pyogenes toxin A protein.
XX KW Tumour; cancer; immune; enterotoxin.
XX OS Streptococcus pyogenes.
XX PN US6180097-B1.
XX PD 30-JAN-2001.
XX PF 30-OCT-1998; 98US-00183437.
XX PR 03-OCT-1989; 89US-00416530.
XX PR 17-JAN-1990; 90US-00466577.
XX PR 17-JAN-1991; 91WO-US000342.
XX PR 01-JUN-1992; 92US-00891718.
XX PR 02-MAR-1993; 93US-00025144.
XX PR 31-JAN-1994; 94US-00189424.
XX PR 19-JUN-1995; 95US-00491746.
XX FA (TERM/) TERMAN D S.
XX PI Terman DS;
XX XX WPI; 2001-158657/16.
XX PT Tumor cell capable of stimulating antitumor immune reactivity in vitro or
XX PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
XX PT costimulatory molecule.
XX PS Disclosure; Fig 2; 16pp; English.
XX CC The present invention relates to a tumour cell capable of stimulating
XX CC antitumor immune reactivity in vitro or in vivo contains and expresses an
XX CC exogenous nucleic acid molecule encoding a superantigen or its active
XX CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
XX CC molecule that activates T cells in conjunction with an antigenic
XX CC stimulus. The invention may be used for cancer therapy by stimulating an
XX CC anticancer immune response in vivo or ex vivo
SQ Sequence 221 AA;
Query Match 23.6%; Score 292.5; DB 4; Length 221;
Best Local Similarity 35.1%; Pred. No. 9.3e-21;
Matches 79; Conservative 42; Mismatches 85; Indels 19; Gaps 10;
Qy 16 SELORNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLPKGFFTGHPWYNDLVDLG 72
Db 7 SOLHRSSLVRLQNIYFLYEGDPVTHENVKSVQDQLSHDLIYN---VSGPNVDKLTCLK 63
Qy 73 SKDATNKYKGVLDLYGAYGYQC-AGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWI 131

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Db 64 NOEMATLFGKKNVDYGVVEYHLCLCENAEASACIYGGVTNHEGNHLEIPKKIVVKVSI 123
QY 132 DGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGRKFLYNSDSFGGKVGORGLIVFHSSEG 191
Db 124 DGIQ-SLSPD-IETNKKWTAQELDYKVRKYLTDNKQLYNGP--SKYETGYIKFIPKMK 179
QY 192 STVSVDLFD----AQQYPTLLRIYRDNKTINSENHLHIDLYLT 232
Db 180 ESFWDFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 220

RESULT 97
AAR13206
ID AAR13206 standard; protein; 239 AA.
XX
AC AAR13206;
XX
DT 15-OCT-1991 (first entry)
XX
DE Staphylococcal enterotoxin B.
XX
KW SEB; cancer treatment; pyrogen; tumouricide.
XX
OS Staphylococcus aureus.
XX
PN W09110680-A.
XX
PD 25-JUL-1991.
XX
PF 17-JAN-1990; 90US-00466577.
XX
PR 17-JAN-1990; 90US-00466577.
XX
PA (TERM/) Terman D S.
XX
PI Terman DS;
XX
DR WPI; 1991-237984/32.
XX
PT Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumoricidal activity as
PT Staphylococcal protein A without potential toxic reactions.
PS Disclosure; Fig 1; 74pp; English.
XX
CC SEB was isolated and purified from S.aureus. It can be used for treating
CC cancer, activating cytokine mediators and procoagulant systems,
CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
CC administered intravenously, optionally with ibuprofen to attenuate toxic
CC reaction to SEB. Synthetic polypeptides having structural homology to
CC Staphylococcal exotoxins are claimed, provided the homology includes
CC statistically significant sequence homology, alignment of Cysteine
CC residues and similar hydropathy profiles. See AAR13203-R13211
XX
SQ Sequence 239 AA;

```

```

Query Match 23.6%; Score 292.5; DB 2; Length 239;
Best Local Similarity 34.0%; Pred. No. 1e-20;
Matches 82; Conservative 44; Mismatches 96; Indels 19; Gaps 8;

QY 2 EKSEINEKDLRKKBELQRLNLSNRQIYYNEKAITENKESDDQPLENTLLFKGFTGH 61
Db 1 ESQDPKPDDELHSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWNLDLLVGLGSKDATNKYKGVLYGAYGYQC-----AGGTPNKTACMYGV 111
Db 59 GNYDNRVRFKKNLADKYKDKVDVFGANYYYQCYFSKKTNDINSHQTDKRTCMYGV 118
QY 112 TLHDNRLTEEEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGRKFLYN 171
Db 119 TEHNGQLDKYSLTVRVFEDGK-NLLSPD-VQTNKKKVTQAQELDYLTRHYLVKNKKLYE 176

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QY 172 SDSFGGKVGORGLIVFHSSEGSTVSVDLFDQAQQYPD--TLLRIYRDNKTINSENHLHIDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDLMPAPGDKFDQSKYLNMYNDNKMVDSKDVKIEVY 233
QY 230 L 230
Db 234 L 234

RESULT 98
AAR45014
ID AAR45014 standard; protein; 239 AA.
XX
AC AAR45014;
XX
DT 25-MAR-2003 (revised)
DT 08-JUN-1994 (first entry)
XX
DE Staphylococcal enterotoxin SEB.
XX
KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KW autoimmune disease; toxicity; Protein A; perfusion system.
XX
OS Staphylococcus aureus.
XX
PN W09324136-A1.
XX
PD 09-DEC-1993.
XX
PF 01-JUN-1993; 93WO-US005213.
XX
PR 01-JUN-1992; 92US-00891718.
XX
PA (TERM/) Terman D S.
XX
PA (STON/) STONE J L.
XX
PI Terman DS, Stone JL;
XX
DR WPI; 1993-405418/50.
XX
PT Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
PT in a patient or for the treatment of auto-immune diseases.
XX
PS Disclosure; Fig 1; 90pp; English.
XX
CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer in
CC a patient. These SEs, and homologues of them, can be used as tumoricidal
CC agents for treating cancers and autoimmune disease. They exhibit
CC tumoricidal activity and toxicity identical to that observed for the
CC Protein A perfusion system. They may be administered by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 239 AA;

```

```

Query Match 23.6%; Score 292.5; DB 2; Length 239;
Best Local Similarity 34.0%; Pred. No. 1e-20;
Matches 82; Conservative 44; Mismatches 96; Indels 19; Gaps 8;

QY 2 EKSEINEKDLRKKBELQRLNLSNRQIYYNEKAITENKESDDQPLENTLLFKGFTGH 61
Db 1 ESQDPKPDDELHSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWNLDLLVGLGSKDATNKYKGVLYGAYGYQC-----AGGTPNKTACMYGV 111
Db 59 GNYDNRVRFKKNLADKYKDKVDVFGANYYYQCYFSKKTNDINSHQTDKRTCMYGV 118
QY 112 TLHDNRLTEEEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGRKFLYN 171
Db 119 TEHNGQLDKYSLTVRVFEDGK-NLLSPD-VQTNKKKVTQAQELDYLTRHYLVKNKKLYE 176
QY 172 SDSFGGKVGORGLIVFHSSEGSTVSVDLFDQAQQYPD--TLLRIYRDNKTINSENHLHIDLY 229

```

Db 177 FNN--SPYETGYIKFIENENG-FWYDLMAPGDKFDQSKYLMNNDKQVDSKDVKIEVY 233

Qy 230 L 230

Db 234 L 234

RESULT 99

AA92319

ID AAY92319 standard; protein; 266 AA.

XX

AC AAY92319;

XX

DT 10-AUG-2000 (first entry)

XX

DE Plant-optimized mutant staphylococcal enterotoxin B.

XX

KW Rep; replicase; rescue; replication; vector; gene expression;

KW recombinant protein production; plant; intronless; enterotoxin B.

XX

OS Staphylococcus sp.

OS Synthetic.

XX

FN WO200020557-A2.

XX

PD 13-APR-2000.

XX

PF 07-OCT-1999; 99WO-US0233520.

XX

PR 07-OCT-1998; 98US-0103352P.

XX

PA (UYCO-) UNIV CORNELL BOYCE INST PLANT RES.

XX

XX Mason HS, Palmer KE, Mor TS, Hefferon KL, Arntzen C;

PI WPI; 2000-303756/26.

XX

DR N-ESDB; AAA09240.

XX

XX

PT Nucleic acids comprising a portion of a long intergenic region of a

PT geninivirus genome and a sequence comprising a geninivirus replicase

PT gene, useful for amplifying a gene of interest and overproducing a

PT protein of interest in plants.

XX

PS Example 17; Fig 36; 121pp; English.

XX

XX A pair of nucleic acids comprising a portion of a long intergenic region

CC (LIR) of a geninivirus genome lacking a sequence encoding a geniniviral

CC coat protein, and a nucleic acid comprising a geniniviral replicase gene

CC linked to a fruit ripening-dependent promoter, are new. Strains of

CC Escherichia coli and Agrobacterium tumefaciens transfected with an

CC expression vector containing the nucleic acids and a gene of interest are

CC useful for the production of transgenic plants (or cells). The sequences

CC and methods are useful for amplifying a gene of interest and

CC overproducing a protein of interest in recombinant plants

XX

SQ Sequence 266 AA;

Query Match 23.6%; Score 292.5; DB 3; Length 266;

Best Local Similarity 33.2%; Pred. No. 1.2e-20;

Matches 81; Conservative 47; Mismatches 97; Indels 19; Gaps 8;

Qy 1 SEKSEINEKDLRKSELRNLSNLROIYYVNEKAITENKESDDQPLENTLLPKGPFPTG 60

Db 27 AESQDPKPEDELHKSSKF-TGLMENMKVLYDDNHVSAT-NVKSIDQSIFYDLIYSIKDTK 84

Qy 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTNKTACMYGG 110

Db 85 LGNYDNRVFEKPKDLADKYDKYDVDFGANYGYCYPSKKTNDINSHTDKRKTCTMYGG 144

Qy 111 VTLHDNRLTBEKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHVLHGKFLY 170

Db 145 VTEHNGNOLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLY 202

Qy 171 NSDSFGKQVORGLIVFHSSSEGSTVSYDLFDAQQGYPD--TLRLRYRONKNTINSENHLIDL 228

Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMNNDKQVDSKDVKIEV 259

Qy 229 YLYT 232

Db 260 YLYT 263

RESULT 100

ABU62453

ID ABU62453 standard; protein; 266 AA.

XX

AC ABU62453;

XX

DT 27-AUG-2003 (first entry)

XX

DE S. aureus periplasmic enterotoxin B mutant E67Q.

XX

KW SEB; staphylococcal enterotoxin B; mutein; mutant; vaccine;

KW superantigen toxin; MHC; superantigen-associated bacterial infection;

KW bacterial infection; antibacterial.

XX

OS Staphylococcus aureus.

OS Synthetic.

XX

FX Key Location/Qualifiers

FT Peptide 1..26

FT Protein /label= Signal_peptide

FT /label= Mature_SEB_mutant

FT Misc-difference 93

FT /note= "Wild-type Glu substituted by Gln"

XX

XX US2003036644-A1.

XX

PD 20-FEB-2003.

XX

XX 26-NOV-2001; 2001US-00002784.

XX

PR 25-JUN-1997; 97US-00882431.

PR 01-SEP-1998; 98US-00144776.

XX

PA (ULRI/) ULRICH R G.

XX

PI Ulrich RG;

XX

XX WPI; 2003-492125/46.

DR

PT New superantigen toxin DNA fragment, useful for preparing a composition

PT for treating or preventing bacterial infection.

XX

PS Example 2; Page; 69pp; English.

XX

CC The invention relates to an isolated and purified superantigen toxin DNA

CC fragment is altered so that binding of the encoded altered toxin to

CC either the MHC class II or T cell antigen receptor is altered. Also

CC included are a recombinant DNA construct (comprising a vector and an

CC isolated and purified altered superantigen toxin DNA fragment), a host

CC cell transformed with the recombinant DNA construct, producing altered

CC superantigen toxin, an altered TST-1 (toxic shock syndrome toxin)

CC superantigen toxin peptide, diagnosing superantigen-associated bacterial

CC infection, a vaccine (comprising an altered superantigen toxin for

CC producing antigenic and immunogenic response resulting in the protection

CC of a mammal against superantigen-associated bacterial infection);

CC treating/ameliorating a superantigen-associated bacterial infection, an

CC antisera isolated from individuals immunised with one or more altered

CC TST-1 superantigen toxin and an antibody which recognises altered TST-

CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,

CC SEB, SECI) and streptococcal pyrogenic enterotoxin a and b (SPEa and

CC SPBb). The superantigen toxin DNA fragment is useful for preparing a

CC composition for treating or preventing bacterial infection. The present

CC sequence represents the E67Q (with reference to the mature protein

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 11:00:34 ; Search time 15 Seconds
(without alignments)
1494.567 Million cell updates/sec

Title: US-09-900-766-7

Perfect score: 1238

Sequence: 1 SEKSEINEKDLRKKSELR.....RDNKTINSENLHLYLVT 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	100.0	257	2 A28179	enterotoxin E prec
2	1023	82.6	257	2 A28564	enterotoxin A prec
3	994	80.3	280	2 C89984	enterotoxin P [imp
4	663	53.6	258	2 A33953	enterotoxin D prec
5	461.5	37.3	258	2 H89968	enterotoxin Sen [i
6	387.5	31.3	260	2 E89969	enterotoxin SeO [i
7	339.5	27.4	242	2 C89969	extracellular ente
8	337	27.2	240	2 G89991	extracellular ente
9	320	25.8	239	2 D89969	enterotoxin SEM [i
10	300.5	24.3	266	1 ENSAB6	enterotoxin B prec
11	295.5	23.9	251	1 S29659	exotoxin type A pr
12	285.5	23.1	266	2 S11885	enterotoxin C3 - S
13	281.5	22.7	266	2 A60114	enterotoxin C-2 pr
14	279.5	22.6	236	2 S18789	exotoxin A precurs
15	277.5	22.4	236	2 S18783	exotoxin type A pr
16	272.5	22.0	236	2 S18786	exotoxin type A pr
17	266.5	21.5	266	1 ENSAC1	enterotoxin C-1 pr
18	255.5	20.6	258	2 G89968	extracellular ente
19	245	19.8	250	1 A26152	streptococcal pyro
20	201	16.2	157	2 A89942	hypothetical prote
21	197	15.9	136	2 A89969	enterotoxin YENT2
22	183.5	14.8	235	2 A30509	exotoxin C precurs
23	144	11.6	62	2 H89941	hypothetical prote
24	123	9.9	133	2 H89969	enterotoxin Yent1
25	113	9.1	232	2 F89807	exotoxin 13 [impor
26	107.5	8.7	234	1 XCSAS1	toxic shock syndro
27	105.5	8.5	234	2 H89992	toxic shock syndro
28	101	8.2	232	2 E89807	exotoxin 12 [impor
29	99.5	8.0	231	2 D89807	exotoxin 11 [impor

30	96	7.8	227	2 G89807	exotoxin 14 [impor
31	94.5	7.6	291	2 G86903	cell shape determi
32	94.5	7.6	631	2 S70908	transferrin-binding
33	94	7.6	203	2 C89803	hypothetical prote
34	94	7.6	226	2 C89806	exotoxin 6 [impor
35	93	7.5	1419	1 DVZQF	multidrug resistan
36	91	7.4	853	2 G90559	tree-like protein
37	90.5	7.3	194	2 AC1553	B. subtilis YjBK p
38	90	7.3	411	2 A11161	flagellar hook pro
39	90	7.3	411	2 A11520	flagellar hook pro
40	90	7.3	5005	2 F82884	hypothetical prote
41	89	7.2	679	2 G71615	phospholipase A2-1
42	89	7.2	1634	2 C89888	DNA-directed DNA p
43	88	7.1	241	2 C89888	hypothetical prote
44	88	7.1	617	2 E96793	hypothetical prote
45	88	7.1	672	1 S73438	MG032 homolog B01
46	87.5	7.1	241	2 T07067	beta-fructofuranos
47	87.5	7.1	556	2 A11394	arginyl tRNA synth
48	87.5	7.1	1014	2 H71602	protein with DnaJ
49	87	7.0	476	2 H82177	conserved hypothet
50	87	7.0	2167	2 AF1489	cell wall-associat
51	86.5	7.0	856	2 B81399	probable periplasm
52	86.5	7.0	1751	2 A45604	major blood-stage
53	86	6.9	630	2 S78650	DNA endonuclease a
54	86	6.9	1090	2 AG1749	glycosidase homolo
55	86	6.9	1353	2 T27404	hypothetical prote
56	85.5	6.9	556	2 AD1770	arginyl tRNA synth
57	85	6.9	614	2 D86342	hypothetical prote
58	85	6.9	617	2 T10102	diphosphate-fructo
59	85	6.9	1902	1 B44858	lactocapin (EC 3.4
60	84.5	6.8	509	2 S73660	ABC transporter, P02
61	84.5	6.8	573	2 AH1793	MG288 homolog P02
62	84.5	6.8	2441	2 D71623	erythrocyte membra
63	84	6.8	227	2 C89808	exotoxin 15 [impor
64	84	6.8	272	2 D86671	transposase of IS1
65	84	6.8	492	2 F70339	glycerol kinase -
66	84	6.8	552	2 T41863	chitinase chi-A or
67	84	6.8	668	2 T44118	penicillin-binding
68	84	6.8	668	2 JQ0773	penicillin-binding
69	84	6.8	668	2 JQ0774	penicillin-binding
70	84	6.8	1014	2 T30545	major surface glyc
71	83.5	6.7	319	2 C81390	hypothetical prote
72	83.5	6.7	324	2 T03276	GAG protein - yeas
73	83.5	6.7	507	2 S36595	li protein - human
74	83.5	6.7	573	2 AF1418	ABC transporter, A
75	83.5	6.7	819	1 I83350	outer membrane ush
76	83	6.7	272	2 C86884	transposase of IS1
77	83	6.7	379	2 C83996	hypothetical prote
78	83	6.7	381	2 C83986	hypothetical prote
79	83	6.7	464	2 A71509	probable transcrip
80	83	6.7	478	2 F90497	hypothetical prote
81	83	6.7	631	2 S70910	transferrin-bindin
82	83	6.7	819	2 G69801	hypothetical prote
83	83	6.7	280	2 E71604	hypothetical prote
84	82.5	6.7	247	2 E97118	uncharacterized pr
85	82.5	6.7	292	2 B89807	exotoxin 9 [impor
86	82.5	6.7	315	2 C64716	rare lipoprotein A
87	82.5	6.7	328	2 F64187	p-aminobenzoate sy
88	82.5	6.7	333	2 F91273	hypothetical secre
89	82.5	6.7	609	2 F90160	membrane conserv
90	82.5	6.7	638	2 AH0340	putative autocransp
91	82.5	6.7	726	2 AB0122	probable ferric si
92	82	6.6	520	2 D83845	hypothetical prote
93	82	6.6	631	2 S55243	upiquitin-like pro
94	82	6.6	756	2 T05829	hypothetical prote
95	82	6.6	2910	2 T28156	DNA-directed RNA p
96	82	6.6	6486	2 T31076	tyrocidine synthet
97	81.5	6.6	356	2 A89807	exotoxin 8 [impor
98	81.5	6.6	616	1 A40457	replication protei
99	81.5	6.6	804	2 G90571	hypothetical prote
100	81.5	6.6	1378	2 G88637	protein F53H1.4 [i
101	81.5	6.6	1553	2 T18502	hypothetical prote
102	81.5	6.6	1711	2 T18429	hypothetical prote

103 81.5 6.6 1883 2 G82875
104 81.5 6.6 2870 2 H96974
105 81 6.5 299 2 A1193
106 81 6.5 333 2 A95982
107 81 6.5 402 2 A92340
108 81 6.5 528 2 S23207
109 81 6.5 562 2 S01312
110 81 6.5 580 2 S49308
111 81 6.5 616 2 A36094
112 81 6.5 626 2 B98115
113 81 6.5 1021 2 A40805
114 81 6.5 1217 2 T21403
115 81 6.5 1561 2 S06839
116 81 6.5 1997 2 F71607
117 81 6.5 2144 2 A97942
118 81 6.5 2485 1 H71621
119 80.5 6.5 261 2 A84077
120 80.5 6.5 344 2 C81920
121 80.5 6.5 413 2 S95650
122 80.5 6.5 993 2 A97334
123 80.5 6.5 1151 2 A45226
124 80.5 6.5 1427 2 S22695
125 80.5 6.5 1520 2 T23620
126 80.5 6.5 1959 2 A61085
127 80 6.5 276 2 T12558
128 80 6.5 1008 2 T18508
129 80 6.5 1231 2 S70553
130 80 6.5 1388 2 T38720
131 80 6.5 1902 2 S06997
132 79.5 6.4 156 2 A0817
133 79.5 6.4 243 2 H71082
134 79.5 6.4 344 2 B1183
135 79.5 6.4 358 2 G84550
136 79.5 6.4 532 2 C97228
137 79.5 6.4 556 2 C72204
138 79.5 6.4 637 2 S36523
139 79.5 6.4 677 2 D82870
140 79.5 6.4 1211 2 D64702
141 79.5 6.4 1392 2 A43336
142 79.5 6.4 2269 2 T18472
143 79.5 6.4 2894 2 C64474
144 79 6.4 348 2 F96997
145 79 6.4 368 2 A82148
146 79 6.4 378 2 F64446
147 79 6.4 419 2 H81667
148 79 6.4 426 2 B97126
149 79 6.4 628 2 A23393
150 79 6.4 660 2 S70904
151 79 6.4 745 2 D82568
152 79 6.4 788 2 A71076
153 79 6.4 1104 2 A60999
154 79 6.4 1131 2 T19442
155 79 6.4 1902 2 B45764
156 79 6.4 2183 2 T42764
157 79 6.4 4981 2 T18489
158 78.5 6.3 259 2 B82348
159 78.5 6.3 318 2 T38919
160 78.5 6.3 627 2 G37975
161 78.5 6.3 722 2 E71403
162 78.5 6.3 781 2 T36143
163 78.5 6.3 836 2 A90540
164 78.5 6.3 998 2 I41078
165 78 6.3 416 2 A11760
166 78 6.3 476 2 G90512
167 78 6.3 626 2 E95250
168 78 6.3 669 2 T05212
169 78 6.3 681 2 F69295
170 78 6.3 692 2 B64381
171 78 6.3 993 2 A81905
172 78 6.3 1091 2 A11380
173 78 6.3 2013 2 C71610
174 77.5 6.3 241 2 B98888
175 77.5 6.3 252 2 E95884

hypothetical prote
cyclic beta 1-2 gl
hypothetical prote
hypothetical prote
probable carboxyl-
DNA-directed RNA p
alpha-amylase (EC
beta-fructofuranos
diphosphate-fructo
hypothetical prote
collagenase - Clos
hypothetical prote
surface antigen sp
DNA helicase II BR
metalloproteinase
serine/threonine-s
transposase (O6) B
hypothetical prote
hypothetical prote
hypothetical prote
type II restrictio
integrin alpha-1 c
restin - human
hypothetical prote
hypothetical prote
porin - common ice
hypothetical prote
chromosome-associ
chromodomain helic
lactocepin (EC 3.4
bacterioferritin c
hypothetical prote
copper ABC transpo
hypothetical prote
hypothetical prote
probable peptide A
alpha-amylase - Th
EI protein - human
DNA topoisomerase
DNA polymerase III
microtubule-vesicl
hypothetical prote
hypothetical prote
uncharacterized co
chorismate synthas
transcription term
cystathionine beta
hypothetical prote
transferrin-bindin
conserved hypotet
hypothetical prote
alpha-amylase (EC
hypothetical prote
lactocepin (EC 3.4
coagulation factor
hypothetical prote
probable lipopolys
conserved hypotet
hypothetical prote
hypothetical prote
probable secreted
outer-membrane fim
hemolysin - Escher
B. subtilis YvLB p
P60-like (mycoplas
glycosyl hydrolase
hypothetical prote
acetyl-CoA synthet
hypothetical prote
outer membrane sec
glycosidase homolo
probable membrane
hypothetical prote
hypothetical prote

176 77.5 6.3 361 2 E86692
177 77.5 6.3 372 2 G96933
178 77.5 6.3 419 1 C53312
179 77.5 6.3 429 2 A25145
180 77.5 6.3 467 2 G69849
181 77.5 6.3 522 2 D96913
182 77.5 6.3 547 2 S49815
183 77.5 6.3 554 2 S41526
184 77.5 6.3 581 2 T51580
185 77.5 6.3 590 2 H70130
186 77.5 6.3 609 2 T32302
187 77.5 6.3 707 2 S78538
188 77.5 6.3 709 2 A41976
189 77.5 6.3 817 2 F86742
190 77.5 6.3 1269 2 A90267
191 77.5 6.3 1325 1 S73723
192 77.5 6.3 3206 1 GNVSPV
193 77 6.2 421 2 A11112
194 77 6.2 425 2 T43772
195 77 6.2 500 2 B43577
196 77 6.2 620 2 E90575
197 77 6.2 646 2 H95155
198 77 6.2 797 2 D71621
199 77 6.2 876 2 A89944
200 77 6.2 893 2 S64926

N-acetylmuramoyl-L
HD-GYP hydrolase d
thymidine phosphor
keratin, 47K type
endo-1,4-beta-xyla
Gipase, sulfate ad
transferrin-bindin
hemolysin accessor
ovule development
oligodeopeptidase
hypothetical prote
site-specific reco
structure-specific
ribonuclease (impo
proteinase related
probable lipoprote
genome polypoteine
hypothetical prote
hypothetical prote
perfringolysin O p
lipoprotein (impor
prolyl oligopeptid
hypothetical prote
alanyl-tRNA synthe
probable membrane

ALIGNMENTS

RESULT 1

A28179
enterotoxin E precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: A28179
R:Couch, J.L.; Soltis, M.T.; Betley, M.J.
A:Title: Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.
A:Reference number: A28179; MUID:88257005; PMID:3384800
A:Accession: A28179
A:Molecule type: DNA
A:Residues: 1-257 <COU>
A:Cross-references: UNIPROT:P12993; GB:M21319; NID:g153001; PIDN:AAA26617.1; PID:g153002
C:Superfamily: enterotoxin B

Query Match 100.0%; Score 1238; DB 2; Length 257;

Best Local Similarity 100.0%; Pred. No. 1.8e-93; Indels 0; Gaps 0;
Matches 233; Conservative 0; Mismatches 0;

Qy 1 SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
Qy 61 HPWYNDLLVDLGSKDATNKYKGVLDYGYAYGQCAGGTPNKTCAMYGVTLDHNNRLT 120
Db 85 HPWYNDLLVDLGSKDATNKYKGVLDYGYAYGQCAGGTPNKTCAMYGVTLDHNNRLT 144
Qy 121 EEKVPINLWDGQTTVPIDKVTSKETVTVQELDLQARHYLHGKFLYNSDSFGGKVQ 180
Db 145 EEKVPINLWDGQTTVPIDKVTSKETVTVQELDLQARHYLHGKFLYNSDSFGGKVQ 204
Qy 181 RGLVFFHSSEGSTVSVDLFDAGQGYPTDLRIYRDNKNTINSENHLDLYLTT 233
Db 205 RGLVFFHSSEGSTVSVDLFDAGQGYPTDLRIYRDNKNTINSENHLDLYLTT 257

RESULT 2

A28664
enterotoxin A precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: A28664; A29566

R:Betley, M.J.; Mekalanos, J.J.
 J. Bacteriol. 170, 34-41, 1988
 A:Title: Nucleotide sequence of the type A staphylococcal enterotoxin gene.
 A:Reference number: A28664; MUID:88086892; PMID:3335483
 A:Accession: A28664
 A:Molecule type: DNA
 A:Residues: 1-257 <BET>
 A:Cross-references: UNIPROT:P13163; GB:M18970; NID:g153120; PIDN:AAA26681.1; PID:g153121
 A:Experimental source: strain BR1337
 R:Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.
 J. Biol. Chem. 262, 7006-7013, 1987
 A:Title: Complete amino acid sequence of staphylococcal enterotoxin A.
 A:Reference number: A29566; MUID:87222293; PMID:3584106
 A:Accession: A29566
 A:Molecule type: protein
 A:Residues: 25-241, 'S', 243-257 <HUA>
 C:Genetics:
 A:Gene: entA
 A:Map position: 6
 C:Superfamily: enterotoxin B

Query Match 82.6%; Score 1023; DB 2; Length 257;
 Best Local Similarity 82.0%; Pred. No. 5.9e-76;
 Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 61 HPWYNDLLVDLGSKDNTNKKYKGVLDYGYAGYQACGTPNKTCMYGGVTLHDNNRLT 120
 DB 85 HSWYNDLLVDFDSKIDVYKGVLDYGYAGYQACGTPNKTCMYGGVTLHDNNRLT 144

QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
 DB 145 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204

QY 181 RGLIVFHSSEGSTVSYDLFDAQGVPTLLRIYRDNKNTINSENHLHIDLYLT 233
 DB 205 RGLIVFHTSTEPSVNYDLFCAQGVPTLLRIYRDNKNTINSENHWIDLYLT 257

RESULT 3
 C89984
 enterotoxin p [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C:Accession: C89984
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, M.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: C89984
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-260 <KUR>
 A:Cross-references: UNIPROT:Q99SU3; GB:BA000018; PIDN:BA043036.1; GSPDB:C89984
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: sep
 C:Superfamily: enterotoxin B

Query Match 80.3%; Score 994; DB 2; Length 260;
 Best Local Similarity 79.0%; Pred. No. 1.4e-73;
 Matches 184; Conservative 17; Mismatches 32; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 28 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 87

QY 61 HPWYNDLLVDLGSKDNTNKKYKGVLDYGYAGYQACGTPNKTCMYGGVTLHDNNRLT 120

DB 88 HQWYNDLLVDLGSKDNTNKKYKGVLDYGYAGYQACGTPNKTCMYGGVTLHDNNRLT 147
 QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
 DB 148 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 207

QY 181 RGLIVFHSSEGSTVSYDLFDAQGVPTLLRIYRDNKNTINSENHLHIDLYLT 233
 DB 208 RGLIEFHPSSGSDVGYDLFCAQGVPTLLRIYRDNKNTIKSNMHIYLYTT 260

RESULT 4
 A33953
 enterotoxin D precursor - Staphylococcus aureus
 C:Species: Staphylococcus aureus
 C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
 C:Accession: A33953
 R:Bayles, K.W.; Iandolo, J.J.
 J. Bacteriol. 171, 4799-4806, 1989
 A:Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin I
 A:Reference number: A33953; MUID:89359112; PMID:2549000
 A:Accession: A33953
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-258 <BAY>
 A:Cross-references: UNIPROT:P20723; GB:M28521; NID:g1492109; PIDN:AAB06195.1; PID:g758699
 C:Superfamily: enterotoxin B

Query Match 53.6%; Score 663; DB 2; Length 258;
 Best Local Similarity 54.5%; Pred. No. 1.2e-46;
 Matches 126; Conservative 35; Mismatches 70; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 26 NENIDSVKEKELHKKSELSSTALNNKHSYADKNPIGENKSTGDOFLENTLLYKFFTD 85

QY 61 HPWYNDLLVDLGSKDNTNKKYKGVLDYGYAGYQACGTPNKTCMYGGVTLHDNNRLT 120
 DB 86 LINFEDLLINFNSKEMAHQFKSKNDVYPIRYSINCYGGEIDRTACTYGGVTPHEGNK 145

QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
 DB 146 ERKKIPINLWINGVQKESVSLDKVQTDKNVTVOELDLQARHYLQKDLKLYNNDTLGGKIQ 205

QY 181 RGLIVFHSSEGSTVSYDLFDAQGVPTLLRIYRDNKNTINSENHLHIDLYLT 231
 DB 206 RKIEFDSSDGSKSVYDLFDVKGDFPEKQLRIYSDNKTLSHHLHIDLYLT 256

RESULT 5
 H89968
 enterotoxin SeN [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C:Accession: H89968
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, M.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: H89968
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-258 <KUR>
 A:Cross-references: UNIPROT:Q9EZM4; GB:BA000018; PIDN:gl3701618; PIDN:BA042911.1; GSPDB:C89968
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: sen
 C:Superfamily: enterotoxin B

Query Match 37.3%; Score 461.5; DB 2; Length 258;

Best Local Similarity 41.2%; Pred. No. 3.1e-30;
Matches 96; Conservative 45; Mismatches 77; Indels 15; Gaps 6;

Qy 6 EINEKLRKKSELRNALSRLRQIYYNEKAIT-----ENKESDDQFLENTLLFKGFFTG 60
Db 32 EVDKKDLKKSELDSSKLFNITS--YYTD--ITWQDESNNKISTDQLLNNTIILNKIDIS 87

Qy 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 88 VLKTSLSKVEFNSSDLANQPKGNIDYGLFGNKCVELTEKTSCLYGGVTHDGNQLD 147

Qy 121 BEKKVPINLWIDGQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 180
Db 148 BEKVGIVNVFQGVQOEGFV--IKTKKAKVTVOELDTKVRFKLENLYKIYNKDT--GNIQ 203

Qy 181 RGLVPHS--SEGSTSVSDLPDAQOQYPTLLRIYRDNKTINSENHLIDLVL 231
Db 204 KGCIFFHSHNHQDSFYDLYNVKSGVGAEPFQFYSDNRVTSSSNYHIDVELY 256

RESULT 6
E89969
enterotoxin SeO [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: E89969
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: E89969
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-260 <KUR>
A:Cross-references: UNIPROT:Q99T46; GB:BA000018; PID:g13701623; PIDN:BA842916.1; GSPDB:G89969
A:Experimental source: strain N315
C:Genetics:
A:Gene: seo
C:Superfamily: enterotoxin B

Query Match 31.3%; Score 387.5; DB 2; Length 260;
Best Local Similarity 39.9%; Pred. No. 3.3e-24;
Matches 97; Conservative 31; Mismatches 86; Indels 29; Gaps 8;

Qy 8 NEKD-----LRKSELRNALSRLRQIYYNE-----KAITENKESDDQFLENTLLFKGFF 58
Db 29 NEEDPKIESLCKSSVDPIALHNINDDYINNRFTTVKSIIVSTTE---KFLDFDLFKSI- 84

Qy 59 TGHPW-----YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGV 111
Db 85 ---NWLDSIAEFKDLKVEFSSAISKEFLGKTVDIYGYVYKAHCHGBHQVDTACTYGGV 141

Qy 112 TLHDNNRLTEKKVPINLWIDGQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYN 171
Db 142 TPHENKLSPEKNIGVAVYKDNVNVNTFI--VTDDKKVTAQELDVKVTKLNAYKLY- 198

Qy 172 SDSFGGKVQRLGVPHSSEGSTSVS--YDLFDAQOQYPTLLRIYRDNKTINSENHLIDL 229
Db 199 -DRMTSDVQKGIKPHSHSEHKESFYDLYFKGNLPDQYLIQYNDNKTIDSSYHIDVY 257

Qy 230 LYT 232
Db 258 LFT 260

RESULT 7
E89969
extracellular enterotoxin type I precursor [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: E89969

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: E89969
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-242 <KUR>
A:Cross-references: UNIPROT:O85383; GB:BA000018; PID:g13701621; PIDN:BA842914.1; GSPDB:G89969
A:Experimental source: strain N315
C:Genetics:
A:Gene: sei
C:Superfamily: enterotoxin B

Query Match 27.4%; Score 339.5; DB 2; Length 242;
Best Local Similarity 35.6%; Pred. No. 2.5e-20;
Matches 79; Conservative 36; Mismatches 74; Indels 33; Gaps 7;

Qy 23 LSNLRQIY---YVNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATN 78
Db 30 VGNLRFYTKHDYIDLKGVTDKNLPANQLE-----FSTG---TNDLISESNWDEIS 79

Qy 79 KYGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGQTTVP 138
Db 80 KFKGKLDIFGIDYNGPC-----KSKVYGGATL-SQYLSNARKIPINLWVNGKHKTI 132

Qy 139 PIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFG-GK-----VQRLVLP 186
Db 133 STDKIATNKKLVTAQELDVKLRYLQBEYNIYGHNTGKGKEYGYSKFYSGFNNGKVL 192

Qy 187 HSSEGSTSVSDLPDAQOQYPTLLRIYRDNKTINSENHLIDL 228
Db 193 HLNNEKSFSDLFTYTGGLPVSFLKIYEDNKIIESEKFHLDV 234

RESULT 8
G89991
extracellular enterotoxin L [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G89991
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: G89991
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-240 <KUR>
A:Cross-references: UNIPROT:Q9F0L7; GB:BA000018; PID:g13701803; PIDN:BA843096.1; GSPDB:G89991
A:Experimental source: strain N315
C:Genetics:
A:Gene: sel
C:Superfamily: enterotoxin B

Query Match 27.2%; Score 337; DB 2; Length 240;
Best Local Similarity 35.3%; Pred. No. 3.9e-20;
Matches 78; Conservative 37; Mismatches 72; Indels 34; Gaps 6;

Qy 25 NLROIY---YVNEKAITENKESDDQFLENTLLFKGFFTGHPWYND--LLVDLGSKDATNK 79
Db 32 NLRNFYTKYEVNLSKNVKNKNSPESHLE-----YSYKNDTLAYAFDEHYETSD 80

Qy 80 YGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGQTTVP 139
Db 81 LKGNVDVFGISYKY---GSNSRT--IYGGVTKAENNKLDSPRIIPINLINGKHQVTV 134

Qy 140 IDKVKTSKKEVTVOELDQARHYLHGKFGLY-----NSDSFGGKVQRLVLP 187

R.; Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3511-3517, 1970
A; Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, composition and properties of the toxin.
A; Reference number: A92064; PMID:71007901; PMID:5470820
A; Contents: annotation; chymotryptic peptides
R.; Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3493-3510, 1970
A; Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, composition and properties of the toxin.
A; Reference number: A92063; PMID:71007900; PMID:5470819
A; Contents: annotation; tryptic peptides
R.; Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.; Dunnery, D.A.; Bergdoll, M.S. Biochemistry 4, 1011-1016, 1965
A; Title: Purification of staphylococcal enterotoxin B.
A; Reference number: A90548; PMID:56035792; PMID:4953912
A; Contents: annotation; biological source of protein
R.; Alakhov, V.Y.; Klinisky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Svishniuk, J. J. Biochem. 209, 823-828, 1992
A; Title: Identification of functionally active fragments of staphylococcal enterotoxin B. A; Reference number: S27240; PMID:93049338; PMID:1425690
A; Accession: S27240
A; Molecule type: protein
A; Residues: 28-42; 128-148 <ALA>
C; Superfamily: enterotoxin B
C; Keywords: enterotoxin; extracellular protein; toxin
F; 1-27/Domain: signal sequence #status predicted <SIG>
F; 28-286/Product: enterotoxin B #status experimental <MAT>
F; 120-140/Disulfide bonds: #status experimental

Query Match 24.3%; Score 300.5; DB 1; Length 266;
Best Local Similarity 33.6%; Pred. No. 4.2e-17;
Matches 82; Conservative 47; Mismatches 96; Indels 19; Gaps 8;

Qy 1 SEKSEEINEKDRLKKSELQRNALSNLRQIYYYNKEATENKESDDQPLENTLLFKGFPTG 60
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
27 AESQPDPKPDELHKSSKF-TGLMENMKVLYDNHVSAL-NVKSIDQFLYFDLIYSIKDTPK 84
Qy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 HPWYNLLVDLGSQDATNKGKVDLYGAYGYQC-----AGTPNKTACMYGG 110
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
85 LGHYNDYRVFFKNQLADKDKVDVFVGANYYYQCYFSKKTINDINSHOTDKRCTCMYGG 144
Qy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
111 VTLDHNRLTEKKVPNLWDIGKQTTPIDKVTSKKEVTVQELDLQARHYLHGKFGLY 170
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
145 VTEHNGNLQKYRSITVRVEDGK-NLLSPD-VQTNKKVTAQELDYLTRHVLVNKKLY 202
Qy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
171 NSDSFGKGQVGLIVFHSSSEGSTSVSYDLFDAOGYPD--TLRIYRDNKNTINSENHLIDL 228
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
203 EPNN--SPYETGIYKFIENENS-FWYDMMPAGDKFDQS KVLWMYNDNMKNQVSKDVIEV 259
Qy : : : : : : : : : : : : : : : : : : : : : : : : : : : :
229 YLYT 232
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
260 YLYT 263
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 260 YLTT 263

RESULT 11

S29659

exotoxin type A precursor (allele 1) - Streptococcus pyogenes phase T12

N;Alternate names: erythrogenic toxin; scarlet fever toxin

C;Species: Streptococcus pyogenes phase T12

C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999

C;Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800

R;Weeks, C.R.; Ferretti, J.J.

Infect. Immun. 52, 144-150, 1986

A;Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) 9c

A;Reference number: S29659; MUID:86166804; PMID:3514452

A;Accession: S29659

A;Molecule type: DNA

A;Residues: 1-251 <WBE>

A;Cross-references: GB:U40453; EMBL:M19350; NID:g1877426; PIDN:AAC48668.1; PID:g1877430

R;Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.

J. Exp. Med. 174, 1271-1274, 1991

A;Title: Characterization and clonal distribution of four alleles of the speA gene encoding

A;Reference number: S18782; MUID:92044323; PMID:1940804

A;Accession: S18782

RESULT 11

S29659
exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12
N:Alternate names: erythrogenic toxin; scarlet fever toxin
C:Species: Streptococcus pyogenes phage T12
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999
C:Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18800
R:Weeks, C.R.; Ferretti, J.J.
Infect. Immun. 52, 144-150, 1986
A:Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) 96
A:Reference number: S29659; MUID:86166804; PMID:35114452
A:Accession: S29659
A:Molecule type: DNA
A:Residues: 1-251 <WBE>
A:Cross-references: GB:U40453; EMBL:M19350; NID:G1877426; PIDN:AAC48868.1; PID:G1877430
R:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene encoded
A:Reference number: S18782; MUID:92044323; PMID:1940804
A:Accession: S18782

Matches	77;	Conservative	43;	Mismatches	92;	Indels	19,	Gaps	10;
QY	4	SEEINEKDLRKKSEIQRNAL-SNLRLQYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG	60						
Db	17	SQEVFQQDPDPSQLHRSSLVNKLQNLYFLYGSDPVTTHENVKSVDQLLSHDLIYN-VS	73						
QY	61	HPMYNDLLVLDGSKAATNKYKGKVDLIGAYGYQC--AGGTPNKTACMGVGTVTLHDNNRL	119						
Db	74	GPNYDKLTGLKNQENATUFDKDNVDIVSYVEYHLCYLCENAERSACIYGGVTNHGHNHL	133						
QY	120	TBEKKVPINLWDGKQTTPIDIKVKTSKEKVTVQELDLQARHYLGKFGYLNSDSFGGVK	179						
Db	134	EIPKKIWKVSIDGIQ-SLSFD-IETNKKMVAQAELDYKVRKYLTDNKQLYTNGP--SKY	189						
QY	180	QRGLIVFHSSSGSTVSVDLFD----AQGYPTDLLRIYRDNKTINSLENLI	226						
Db	190	ETGYIKFIPKNRESFWDFPEFPETQSKY-----LMYKDNETLDSNTSQI	236						
RESULT 17									
ENSAC1									
C;Species:	Staphylococcus aureus								
C;Date:	15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004								
C;Accession:	S06356; A01816								
R;Bohach, G.A.; Schlievert, P.M.									
Mol. Gen. Genet.	209, 15-20, 1987								
A;Title:	Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness t								
A;Reference number:	S06356; MUID:88038352; PMID:2823067								
A;Accession:	S06356								
A;Molecule type:	DNA								
A;Residues:	l-266 <BOH>								
C;Cross-references:	UNIPROT:P01553; EMBL:X05815; NID:g46566; PIDN:CAA29260.1; PID:g46567								
R;Schmidt, J.J.; Spero, L.									
J. Biol. Chem.	258, 6300-6306, 1983								
A;Title:	The complete amino acid sequence of Staphylococcal enterotoxin C-1.								
A;Reference number:	A01816; MUID:83213327; PMID:6189824								
A;Accession:	A01816								
A;Molecule type:	protein								
A;Residues:	28-75, 'IL', 78-176, 'N', 178-266 <SCH>								
C;Genetics:									
A;Gene:	entC1								
C;Superfamily:	enterotoxin B								
C;Keywords:	enterotoxin								
F;1-27/DNA:	signal sequence #status predicted <SIG>								
F;28-266/Product:	enterotoxin C-1 #status experimental								
F;120-137/Disulfide bonds:	#status experimental								
Query Match	21.5%	Score	266.5;	DB 1;	Length	266;			
Best Local Similarity	30.5%;	Pred. No.	2.5e-14;						
Matches	74;	Conservative	51;	Mismatches	101;	Indels	17;	Gaps	8;
QY	1	SEKSEINEKDLRKKSELQRNALSNLRQIYYNEYKAITENKESDDQFLENTLLFKGFFTG	60						
Db	27	AESQPPTDELHKASF-TGLMENMKVIYDDHYVSATKVK-SVDRFLAHDLIYNIISDKK	84						
QY	61	HPMYNDLLVLDGSKAATNKYKGKVDLIGAYGYQC-----AGGTPNKTACMGVGTVL	113						
Db	85	LKNYDKVTTELLNEGLAKKYKDEVVDVYSNVYVCYFSSKDVGNVGTGKTCMYGITK	144						
QY	114	HNNRUTE--KKVPINLMDIGKQTTPIDIKVKTSKEKVTVQELDLQARHYLGKFGELYN	171						
Db	145	HEGNHFEDNGLNQVLIRVV-ENKRNTISP-EVOTDKKSVTAQELDIKARNFLINKNLYE	202						
QY	172	SDSGFGKVGORGLIVPHFSSEGSTVSYDLFDAQGQYPD--TLLRIYRDNKTINSLENLAIDL	229						
Db	203	FNS--SPYETGTYIKFIENNNGTFWDMMPAGDGPDQSCKYLMYNDNKTIVDSKSVIEHV	260						
QY	230	LYT	232						
Db	261	LTT	263						

RESULT 18
G89968
extracellular enterotoxin type G precursor [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G89968
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G89968
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <KUR>
A:Cross-references: UNIPROT:O85382; GB:BA000018; PID:gl3701617; PIDN:BAB42910.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: seg
C:Superfamily: enterotoxin B

Query Match 20.6%; Score 255.5; DB 2; Length 258;
Best Local Similarity 29.1%; Pred. No. 1.9e-13; Mismatches 83; Indels 41; Gaps 11;
Matches 71; Conservative 49

QY 11 DLKKESELQRL--ALSNLRQIYY--YNEKAITENKESDDQFLENTLLFKGFTGHPWYN 65
DB 33 ELNKVSDYKNNKGTGWNVNLTPSPVEGRVINSR----QFLSHDLIFP---IEKSN 85
QY 66 DLLVDLGSKDATNKYKGGKVDLYGAYGYQCA-----GGTPNKATCMYGGVTL 113
DB 86 EVKTELENTLANNYKDKVDIFGVFYTCIIPKSEPDINQNFSG-----CMYGGTLF 140
QY 114 H--DNNLTTEKKVPINLMDGKQITVPIDKVKTSKKEVTVQELDLQARHYLHGKGLN 171
DB 141 NSENER-----DKLITVQVTDNRSLG--FTITNKQNVITQELDYKARHLTKKKGLYE 195
QY 172 SPSFGKVGRLIVFHSRSGSVTSVDFDAQGGYPTD---LLRIYRDNTKNTINSENHIDL 228
DB 196 FD--GSAPESGYIKTEKNTSFWDLPFKKELVPVPYKFLNIYGDNKVDSKSKMEV 253
QY 229 YLYT 232
DB 254 FLNT 257

RESULT 19
A26152
streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.
N:Alternate names: scarlet fever toxin; SPE type A (speA)
C:Species: Streptococcus sp.
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A26152
R:Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.
Mol. Gen. Genet. 203, 354-356, 1986
A:Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Sta
A:Reference number: A26152; MUID:86284313; PMID:3526093
A:Accession: A26152
A:Molecule type: DNA
A:Residues: 1-250 <JOH>
A:Cross-references: UNIPROT:P08095
C:Superfamily: enterotoxin B
C:Keywords: exotoxin

Query Match 19.8%; Score 245; DB 1; Length 250;
Best Local Similarity 30.7%; Pred. No. 1.3e-12;
Matches 70; Conservative 42; Mismatches 94; Indels 22; Gaps 9;

QY 14 KKESELQRLSNLRQIYYNEKA--IT-ENKESDDQFLENTLLFKGFTGHPWYNDLLVD 70
DB 35 KPSQLQSLNLVTKIYIFPMRVTLVTHENVKSDVQLLSDHLLYN---VSGPNYDKLKTE 91

RESULT 20
A89942
hypothetical protein SA1430 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A89942
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89759; MUID:21311952; PMID:11418146
A:Accession: A89942
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-157 <KUR>
A:Cross-references: UNIPROT:Q99TP7; GB:BA000018; PID:gl3701400; PIDN:BAB42694.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1430

Query Match 16.2%; Score 201; DB 2; Length 157;
Best Local Similarity 35.6%; Pred. No. 2.7e-09;
Matches 42; Conservative 21; Mismatches 53; Indels 2; Gaps 2;

QY 1 SKSEINEKDLRKSELRNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
DB 42 TNSAIAEYSDLLHKSKFDSKLSNAK--MSFINPTQL--ENKNTNDRLLKHLDFHDMFVN 99
QY 61 HPWYNDLLVGLSKDATNKYKGGKVDLYGAYGYQCAAGTTPNKATCMYGGVTLHDNR 118
DB 100 VASKKDFKVEFENEALSKKFINKINDIYAGSYSECHGGATNKTQCSGGVTLSDNNK 157

RESULT 21
A89969
enterotoxin YENT2 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A89969
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: A89969
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <KUR>
A:Cross-references: UNIPROT:Q99T49; GB:BA000018; PID:gl3701619; PIDN:BAB42912.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: yent2

Query Match 15.9%; Score 197; DB 2; Length 136;
Best Local Similarity 34.1%; Pred. No. 4.8e-09;
Matches 46; Conservative 28; Mismatches 51; Indels 10; Gaps 5;

QY 103 KTACMYGGVTLHDNRLTEKKV--PINLW----DGQTTVPIDKVKTSKKEVTVQELDL 157

Db 2 KKTGCGVTEHDGNDKNNSTDNHILKVVENERNSLSD-IPNKKKNITAEIDY 60
Qy 158 QARHLYHCKFGLYNSDSFGGKVQRGLIVFHSSEGSTVSYDLFDAQGO--YPTLLRIYRD 215
Db 61 KVRNLLKHKVLYEFNS--SPYETGYIKFIEGSHSFWDLPESGKKFYPTKYLIIYND 118
Qy 216 NKTINSENHLIDLVL 230
Db 119 NKTVESKSINVEVHL 133
RESULT 22
A30509
exotoxin C precursor - Streptococcus pyogenes
C:Species: Streptococcus pyogenes
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: A30509
R:Goshorn, S.C.; Schlievert, P.M.
Infect. Immun. 56, 2518-2520, 1988
A:Title: Nucleotide sequence of streptococcal pyrogenic exotoxin type C.
A:Reference number: A30509; MUID:88314303; PMID:3045005
A:Accession: A30509
A:Molecule type: DNA
A:Residues: 1-235 <GOS>
A:Cross-references: UNIPROT:P13380; GB:M35514; NID:g153820; PIDN:AAA27017.1; PID:g153821
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
Query Match 14.8%; Score 183.5; DB 2; Length 235;
Best Local Similarity 25.8%; Pred. No. 1.2e-07;
Matches 61; Conservative 37; Mismatches 73; Indels 65; Gaps 11;
Qy 47 FLENTLLPKGFFTGH-----PW-YNDLLVGLSGKDA-----TNK 79
Db 11 FIITVILISTFTYHQSDSKDISNVKSDLLAYVITPYDKYDCRVNFSFTHTLINIDTQK 70
Qy 80 YKGG-----KVDLYGAVYGVQCAGGTPNKTACMYGGVTLHDNNRL 119
Db 71 YRGKDYISSEMSVEASQKFRDDHVDVFGLYINSHTG-----EYIGGITPAQNNKV 125
Qy 120 TEKKVPINLMDGKQTTPIDKVKTSKKEVTVOELDLQARHLYHCKFGLYNSDS--FGG 177
Db 126 NH--KLLGNLFISGESQQNNKNIILEKDI VTFQEIDPKIRKLYMDNVIYDATSPYVSG 183
Qy 178 KVQRGLIVFHSSEGSTVSYDLFDA--QQYPTLLRIYRDNKTINSENL-HIDLVL 230
Db 184 RIEIG-----TKQKGHEQIDLDFSPNEGTRSDIFAK-YKDNRIINMKNFSHFDIYL 233
RESULT 23
H89941
hypothetical protein SA1429 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H89941
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H89941
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <KUR>
A:Cross-references: UNIPROT:Q99TP8; GB:BA000018; PID:g13701399; PIDN:BAB42693.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1429
Query Match 11.6%; Score 144; DB 2; Length 62;
Best Local Similarity 39.3%; Pred. No. 3.7e-05;

Matches 22; Conservative 16; Mismatches 18; Indels 0; Gaps 0;
Qy 176 GKGVQRGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNKTINSENHLIDLVL 231
Db 5 GGDIVKGVTKVTHNDDEQNVEYDFNLNGEYGEYEVKMYADNKTINRKHLHDIYLF 60
RESULT 24
B89969
enterotoxin Yent1 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: B89969
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: B89969
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <KUR>
A:Cross-references: UNIPROT:Q99T48; GB:BA000018; PID:g13701620; PIDN:BAB42913.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: Yent1
Query Match 9.9%; Score 123; DB 2; Length 133;
Best Local Similarity 30.0%; Pred. No. 0.005;
Matches 39; Conservative 25; Mismatches 38; Indels 28; Gaps 8;
Qy 3 KSEINEKDLRKSELQORNALNLRIQIYYNEKAITE-NKESDDQFLENTLLFKGFFTGH 61
Db 25 KPEQLN-----KASEF-TGLMDNMR--YLYDDKHVSETNIKSKQKFLQDLELFK--INGS 74
Qy 62 PWYNDLLVGLSGKDATNKYKGGKVDLYGAVYGVQCAGGTPNKTACMYGGVTLHDNNRLTE 121
Db 75 ---KILKTEFPNKSLSKYKKNVDFLFGTNYNQC-----YFSL---DNMELND 117
Qy 122 EKKVPINLMI 131
Db 118 GRLEIKNVYV 127
RESULT 25
F89807
exotoxin 13 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: F89807
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: F89807
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-232 <KUR>
A:Cross-references: UNIPROT:Q99WH4; GB:BA000018; PID:g13700319; PIDN:BAB41617.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: set13
C:Superfamily: toxic shock syndrome toxin
Query Match 9.1%; Score 113; DB 2; Length 232;
Best Local Similarity 24.5%; Pred. No. 0.065;
Matches 59; Conservative 29; Mismatches 79; Indels 74; Gaps 12;
Qy 17 ELQRNALNLRIQIYYNEKAITEN--KESDDQFLENTL-----LFKGFFTGHFWYNDL 67


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Db 36 ETQRKYINMLHQQYSEBSFESTNISVKSSEDYVGNVLNFNQNKTKFKVLLG----- 88
Qy 68 LVDLGSKDATNKYKGGK-----VDLYGATYGYQCAGTGNKTKACMYGGVTLDHN 116
Db 89 -----DDKNKYKEKTHGLDVPFAPVELLDIKGGI--YVGGITKKNVSFGFV---S 135
Qy 117 NRLTEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGFLYNSDSFG 176
Db 136 NPSLQVKKV-----DAKHGFSINELPFTQKEVSLKELDFKIRKMLVEKRYLYK----- 184
Qy 177 GKVQGLIVFHSSE-----GSTVSYD-LFDAQGYQPDTLRLIYRDNKTINSENHLHD 227
Db 185 GASDGRIVINMKDEKKYVLDLSEKLSFDRMFDVM-----DSKQI--KNIEVN 230
Qy 228 L 228
Db 231 L 231

RESULT 26
XCSAS1
N:Alternate names: TSST-1
C:Species: Staphylococcus aureus
C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: A24606; D2A606
R:Blomster-Hautamaa, D.A.; Kreiswirth, B.N.; Kornblum, J.S.; Novick, R.P.; Schlievert, H.
J. Biol. Chem. 261, 15783-15786, 1986
A:Title: The nucleotide and partial amino acid sequence of toxic shock syndrome toxin-1.
A:Reference number: A24606; MUID:87057222; PMID:3782090
A:Accession: A24606
A:Molecule type: DNA
A:Residues: 1-234 <BLO>
A:CROSS-references: UNIPROT:P06886; GB:J02615; NID:gi513122; PID:AAA26682.1; PID:gi513123
A:Accession: B24606
A:Molecule type: protein
A:Residues: 41-106;199-224 <BLO2>
A:Note: the authors translated the codon ACT for residue 20 as Ile and GGG for residue 1
C:Superfamily: toxic shock syndrome toxin
C:Keywords: toxic shock syndrome; toxin
F:1-40/Domain: signal sequence #status predicted <SIG>
F:41-234/Product: toxin shock syndrome toxin-1 #status experimental <MAT>

Query Match 8.7%; Score 107.5; DB 1; Length 234;
Best Local Similarity 23.0%; Pred. No. 0.19;
Matches 53; Conservative 35; Mismatches 69; Indels 73; Gaps 12;

Qy 11 DLKKSELOARNLSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVD 70
Db 58 DFTFTSEVLDNSLGSMDR-----IKNTDGSII--SLIIFPS-----PYSPAPT- 97
Qy 71 LGSKDATNKYKGGKVDL-----YGAYGYQCAGGTPNKTACMYGGVTLDHNNR 118
Db 98 -----KGEKVDLNTKTKKSOHTSEGTYIHFOISGVT-----NTEK 133
Qy 119 LTEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGFLY-NSDSFG 176
Db 134 LPTPIELPKVKVHGKDSPLKYGP-KFDKKQLAISTLDPEIRHQLTQIHGLYRSSDKTG 192
Qy 178 --KVQGLIVFHSSEGSTVSVDL---FDAQGYQPDTLRLIYRDNKTINSE 222
Db 193 YWKIT-----MNDGSTVQSDLSKKFVNTKPPINI---DEIKTIEAE 232

RESULT 27
B89992
toxic shock syndrome toxin-1 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: B89992
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi,
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, R.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of .metcillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: B89807
A:Molecule type: DNA
A:Residues: 1-232 <KUR>
A:CROSS-references: UNIPROT:Q99WH5; GB:BA000018; PID:gi13700318; PID:BAB41616.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: set12
C:Superfamily: toxic shock syndrome toxin

Query Match 8.2%; Score 101; DB 2; Length 232;
Best Local Similarity 24.3%; Pred. No. 0.62;
Matches 60; Conservative 33; Mismatches 94; Indels 60; Gaps 11;

Qy 3 KSEENKDLRKSELOARNLSNLRQIYYNEKAITENKESDDQFLENTLLFKGFF 58
Db 24 ENQSVNAKGYEK---MNLVDYTNKLHQYSGPSYELTNVSGSQGYDSDNLLF--- 75
Qy 59 TGHFWNDLLDLGSKDATNKYKGGK-----VDLYGAYGYQCAGGTPNKTACM 107
Db 76 --NQKNQKQFVLLGKD-ENKYKKBKTHGLDVPFAPVELVDLDGRIPS----- 118
Qy 108 YGVTLDHNNRLTEKKVPINLW---IDGKQTTVPIDKVKTSKEVTVQELDLQARHYLH 164
Db 119 VSGVTKKVKSIFESLRTP-NLLVKLIDDKDGSIDEPFFIQKEEYSLKELDFKIRKLLI 177
Qy 165 GKFGLYNSDSFGKQVGRGIVFHSSEGSTVSVDLFDQAQGYQPDTLRLIYRDNKTINSE-- 222
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Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of metcillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: B89992
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-234 <KUR>
A:CROSS-references: UNIPROT:Q54462; GB:BA000018; PID:gi13701806; PID:BAB43099.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: tst
C:Superfamily: toxic shock syndrome toxin

Query Match 8.5%; Score 105.5; DB 2; Length 234;
Best Local Similarity 23.2%; Pred. No. 0.27;
Matches 54; Conservative 35; Mismatches 65; Indels 79; Gaps 13;

Qy 11 DLKKSELOARNLSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVD 70
Db 58 DFTFTSEVLDNSLGSMDR-----IKNTDGSII--SLIIFPS-----PYSPAPT- 97
Qy 71 LGSKDATNKYKGGKVDL-----YGAYGYQCAGGTPNKTACMYGGVTLDHNNR 118
Db 98 -----KGEKVDLNTKTKKSOHTSEGTYIHFOISGVT-----NTEK 133
Qy 119 LTEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGFLY-NSDS 174
Db 134 LPTPIELPKVKVHGKDSPLKYWP---KFDKKQLAISTLDPEIRHQLTQIHGLYRSSDK 189
Qy 175 FGG--KVQGLIVFHSSEGSTVSVDL---FDAQGYQPDTLRLIYRDNKTINSE 222
Db 190 TGGYWKIT-----MNDGSTVQSDLSKKFVNTKPPINI---DEIKTIEAE 232

RESULT 28
B89807
exotoxin 12 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: B89807
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi,
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, R.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of .metcillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: B89807
A:Molecule type: DNA
A:Residues: 1-232 <KUR>
A:CROSS-references: UNIPROT:Q99WH5; GB:BA000018; PID:gi13700318; PID:BAB41616.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: set12
C:Superfamily: toxic shock syndrome toxin

Query Match 8.2%; Score 101; DB 2; Length 232;
Best Local Similarity 24.3%; Pred. No. 0.62;
Matches 60; Conservative 33; Mismatches 94; Indels 60; Gaps 11;

Qy 3 KSEENKDLRKSELOARNLSNLRQIYYNEKAITENKESDDQFLENTLLFKGFF 58
Db 24 ENQSVNAKGYEK---MNLVDYTNKLHQYSGPSYELTNVSGSQGYDSDNLLF--- 75
Qy 59 TGHFWNDLLDLGSKDATNKYKGGK-----VDLYGAYGYQCAGGTPNKTACM 107
Db 76 --NQKNQKQFVLLGKD-ENKYKKBKTHGLDVPFAPVELVDLDGRIPS----- 118
Qy 108 YGVTLDHNNRLTEKKVPINLW---IDGKQTTVPIDKVKTSKEVTVQELDLQARHYLH 164
Db 119 VSGVTKKVKSIFESLRTP-NLLVKLIDDKDGSIDEPFFIQKEEYSLKELDFKIRKLLI 177
Qy 165 GKFGLYNSDSFGKQVGRGIVFHSSEGSTVSVDLFDQAQGYQPDTLRLIYRDNKTINSE-- 222
```

```
Db 178 KKYKLYE-----GSADKGRIVNMKNKDKYBIDLSDK-----LQPERMADVINSQI 224
Qy 223 -NLHIDL 228
Db 225 KNIEVNL 231

RESULT 29
D89807
exotoxin 11 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D89807
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: D89807
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-231 <KUR>
A:Cross-references: UNIPROT:Q99WH6; GB:BA000018; PID:g13700317; PIDN:BA841615.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: set11

Query Match 8.0%; Score 99.5; DB 2; Length 231;
Best Local Similarity 24.0%; Pred. No. 0.82;
Matches 56; Conservative 31; Mismatches 93; Indels 53; Gaps 11;

Qy 2 EKSSEINE-----KDLRKSELQNALSNLR-QIYYN-EKAITENKESDDQFLENTLLPK 55
Db 32 EKQERVQHLVDIKOLYRYSSEFEFSNISKVENYNGSNVRFNQE-----QNHQLF- 85
Qy 56 GFTGHPWYNDLLVDLGSKDATNKYK---GKVDLYGAYGYQCAGGTPNKTACMGVGV 111
Db 86 -----LLGKD-KDKYKGLQGNFVVKELI-----DPNGRLSTVGCV 122
Qy 112 TLHNNRLTEKKVPINLWDGKQTPVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYN 171
Db 123 TKONKSSETNHLFPVK-VYGVNLDSIDSFLINKKEVSLKELDFKIRKQLVEKYGLYK 181
Qy 172 SDSFGKVGQGLIVPHSSEGSTVSVDLFDAGQGPDTLLRYDRNKTINSEN 224
Db 182 -----GTTKYKITINLXDKERKEVIDLGDK-----LQPERMGDVILNSKDI 221

RESULT 30
G89807
exotoxin 14 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G89807
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: G89807
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-227 <KUR>
A:Cross-references: UNIPROT:Q99WH3; GB:BA000018; PID:g13700320; PIDN:BA841618.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: set14
C:Superfamily: toxic shock syndrome toxin

Query Match 7.8%; Score 96; DB 2; Length 227;
```

```
Best Local Similarity 26.7%; Pred. No. 1.5;
Matches 54; Conservative 28; Mismatches 76; Indels 44; Gaps 9;

Qy 8 NEKDRLK--KSELQNALSNLRQIYYNKAITENKESDDQFLENTLLFKGFFTGHPWN 65
Db 33 NQKSVNKHDKAALYR-----YYTGKTMEMKNISALKHGKNNLRFK--FRGIKIQV 80
Qy 66 DLLVDLGSKDATNKYK-----KKVDLYGAYGYQCAGGT--PNKTACMGVGVTLHDN 116
Db 81 LLPGNDKSKQORSYEGLDVFFVQEKDKHDFY---TVGGVIQNNKTS-----GVVSAPI 133
Qy 117 NRLTEKKVPINLWDGKQTPVPIDKVKTSKEVTVOELDLQARHYLHGKGLYNSDSFG 176
Db 134 LNISKEK-----GEDAPVKGPYPIYKEKITLKELDYKLRKHLIKYGLYKNTISK 184
Qy 177 GKVGQGLIVPHSSEGSTVSVDL 198
Db 185 GRVKISL-----KDGSPYNLDDL 201

RESULT 31
G86903
cell shape determining protein [imported] - Lactococcus lactis subsp. lactis (strain IL1;
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: G86903
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: G86903
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-291 <STO>
A:Cross-references: UNIPROT:Q9CDI9; GB:AE005176; PID:g12725299; PIDN:AAK06329.1; GSPDB:G
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: mreC

Query Match 7.6%; Score 94.5; DB 2; Length 291;
Best Local Similarity 20.7%; Pred. No. 2.8;
Matches 48; Conservative 26; Mismatches 67; Indels 91; Gaps 8;

Qy 21 NALSNLRQIYYNKAIT-----ENK-----ESDDQFLENTLLFKGFFTG----- 61
Db 67 NELSNLMDTYQONQSLKTQLAKSKDDNKLGLSENKELKALKLQETLTDYQTVAAV 126
Qy 62 -----PWYNDLLVDLGSKDATNKYKGGVDLYGAYGYQCAGGTPNKTACMGVGVTLHD 115
Db 127 ITREPSSWNDDTLVIDSGSKD-----GLTTGMIVMANGGV--- 161
Qy 116 NNRLTE-----BKKVPINLWDGKQTPVPIDKVKTSKEVTVOELDLQ 158
Db 162 -GRVTQVNNKSKVALLSSSGIKDNKIPRVIESDGSPIYGLISSVDSQAEAVVKNIDSQ 220
Qy 159 ARHYLHGKFGLYNSDSFGKVGQGLIVPHSSEGSTVSVDLFDAGQGYPTLL 210
Db 221 -----GKFKNGDSVFTSLGINSG-----SQGGTFSGLL 249

RESULT 32
S70908
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB29)
C:Species: Haemophilus influenzae
A:Variety: strain SB29
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S70908; S73321
R;Locmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E.
Mol. Microbiol. 19, 575-586, 1996
A:Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes.
A:Reference number: S70901; MUID:96228706; PMID:8830248
A:Accession: S70908
A:Molecule type: DNA
```

A:Residues: 1-631 <LOO>
A:CROSS-references: UNIPROT:Q48041; EMBL:U15055
A:Experimental source: strain SB29, clone DS-1090-3-2
R:Loosmore, S.M.
submitted to the EMBL Data Library, September 1994
A:Reference number: S73320
A:Accession: S73321
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250, 'L', 252-349, 'RTDATTN', 357-631 <LOW>
A:CROSS-references: EMBL:U15055; NID:G1223948; PIDN:AAAC43931.1; PID:G1223949
A:Experimental source: strain SB29, clone DS-1090-3-2
C:Genetics:
A:Gene: tbp2
A:Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor
P:1-17/Domain: signal sequence #status predicted <SIG>
P:18-631/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 7.6%; Score 94.5; DB 2; Length 631;
Best Local Similarity 20.8%; Pred. No. 7.4;
Matches 52; Conservative 28; Mismatches 55; Indels 115; Gaps 11;

QY 31 YNNEKAITENKESDDQFLENTL-----LPKGP-----FTCHPWYNDL----- 67
DB 202 YNRRSAISDIDN-----LENNLKNAGLTSEFTVNFGTKLTKGLYNERETNNKQLQR 257
QY 68 ---LVDLGSKDATNKYKGK-----KVDLYGAYGYQCAGGTPNKTACMY 108
DB 258 KHELVDIDADIYSNFRGRKVKPTTKDSQEHFTSEGLEGFYG-----PNGE--L 308
QY 109 GGVTLHDNNRL-----TEKKVPINLWIDGKQTTVPIDK-----VKTSKKEV 150
DB 309 GCKFLAGDNRVGFVSKEETKDKLSRETLDGKLIFFTKTKTDAKTAANAKTDEKNF 368
QY 151 TVQELD-----LQARHYLHG-----KFG 168
DB 369 TTKDIPSGEADYLLIDNVFPLFPBENTNDFITSRHHKVGDKTVKVEACCKNLVYVRF 428
QY 169 LYNDSFGGK 178
DB 429 MYEDPLNGE 438

RESULT 33
C99803
hypoetical protein SA0357 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: C89803
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: C89803
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-203 <KUR>
A:CROSS-references: UNIPROT:Q99WK7; GB:BA000018; PID:G13700284; PIDN:BAB41582.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0357

Query Match 7.6%; Score 94; DB 2; Length 203;
Best Local Similarity 21.5%; Pred. No. 1.9;
Matches 51; Conservative 34; Mismatches 52; Indels 100; Gaps 12;

QY 1 SEKSEBINEKDLKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 37 TQNSSVQDKQLQKVEVPNN-----SEKLVKK----- 65
QY 61 HPWYNDLLVGLSKDATNKYKGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRL 119

DB 66 -----LYDRYSKDTIN-----GKSNKSRNWYSEPLNEQ-- 96
QY 120 TEKKVPINLWIDGKQTTVPIDKVKTSKE-----VTQELDLQARHYLHGKFGLYNS 172
DB 97 -----VRIHLEGTYYTA--DRVVTPKRNITLKEVVTLKELDHIR-FAHSYGLY-- 144
QY 173 DSFGKVGORGLIVFHSSEGSTVSYDLFDAQQGYPTL-----LRIYRNKNTINSENL 224
DB 145 --MGEHLPGKGNIVINTKDG-----GKY--TLESHKELQDRENVKINTADI 186

RESULT 34
G89806
exotoxin 6 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G89806
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89759; MUID:21311952; PMID:11418146
A:Accession: G89806
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-226 <KUR>
A:CROSS-references: UNIPROT:Q99WT1; GB:BA000018; PID:G13700312; PIDN:BAB41610.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: set6
C:Superfamily: toxic shock syndrome toxin

Query Match 7.6%; Score 94; DB 2; Length 226;
Best Local Similarity 22.5%; Pred. No. 2.2;
Matches 49; Conservative 38; Mismatches 63; Indels 68; Gaps 11;

QY 8 NEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW---- 63
DB 24 NVQSVQAKTEVKQOSEELK--HYTN-KPVLERN-----VTGYKYTEKG 65
QY 64 --YNDLLVD-----LGS-KDQATNKYKGKVDLYGAYGYQCAGGTPNKTACMYGGVT 112
DB 66 KDYIDVIDVNOYQSQISLVGSDKDKFGDQNSNIDVF-----ILREGDSRQATNYSIGGVT 120
QY 113 LHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKE-----VTQELDLQAR 160
DB 121 -----KTNSQPFIDYIHT--PILEIKKKEEPOSSLYQIYKEDISUKELDYRLR 167
QY 161 HVLHGKFGLYNSDSFGKVGORGLIVFHSSEGSTVSYDL 198
DB 168 ERAIKQHGGLYSNG-----LKQSQIITMKDGKSHITDL 200

RESULT 35
DVZQF
Multidrug resistance protein - malaria parasite (Plasmodium falciparum)
N:Alternate names: P-glycoprotein
C:Species: Plasmodium falciparum
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: S18204; A32547
R:Triglia, T.; Foote, S.J.; Kemp, D.J.; Cowman, A.F.
Mol. Cell. Biol. 11, 5244-5250, 1991
A:Title: Amplification of the multidrug resistance gene pfmdr1 in Plasmodium falciparum
A:Reference number: S18204; MUID:92017800; PMID:1922044
A:Accession: S18204
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1419 <TRI>
A:CROSS-references: UNIPROT:P13568; EMBL:X56851; NID:G9935; PIDN:CAA0180.1; PID:G9936
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1990
R:Foote, S.J.; Thompson, J.K.; Cowman, A.F.; Kemp, D.J.

Query Match	7.3%;	Score 90;	DB 2;	Length 5005;
Best Local Similarity	21.2%;	Pred. No. 2.3e+02;		
Matches 62;	Conservative 40;	Mismatches 113;	Indels 78;	Gaps 12;

RESULT 41
G71615
phospholipase A2-like a/b fold hydrolase PFB0410c - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C:Accession: G71615
R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
.; Perles, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743; PMID:9804551
A:Accession: G71615
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-679 <GAR>
A:Cross-references: UNIPROT:O96176; GB:AE001393; GB:AE001362; NID:G3845175; PIDN:AAC7187
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0410c

C:Species: Plasmodium falciparum
 C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
 C:Accession: G71615
 R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
 ; Partea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
 Science 282, 1126-1132, 1998
 A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
 A:Reference number: A71600; MUID:99021743; PMID:9804551
 A:Accession: G71615
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-679 <GAR>
 A:Cross-references: UNIPROT:O96176; GB:AE001393; NID:g3845175; PIDN:AAC7187
 A:Experimental source: clone 3D7
 C:Genetics:
 A:Gene: PFB0410C

Matches 60; Conservative 40; Mismatches 73; Indels 111; Gaps 15;

Qy 22 ALSNLRQI-YYNEKAITENKESDDQFLENTLFPKGFTGHWPYNDLLVLGSKDATNKY 80
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 275 ALERELRNGVIYEODGATWLTRTDPEDDKORVLIKSOGS-----YTYFLPDIAYH--LNKL 328
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 81 K---KKGVLDLYGA-YYGY-----QCAGTTPNKTACMYGGVTYLHNRRRLTBEEKVPIN 128
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 329 ERGFDVLIDIGWADHHGYIPMRRAAIBALGYSP-----NQLEVEIIQLVH 373
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 129 LWIDGKOTTVPIDKVTSK---KEVT---VOELDLQARHYLHGKFGLYNSDSF----- 175
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 374 LFDGVO-----VKMSKTKGKSVTWRRDLIEVGLOATRYF---FAWRSDTHMFMDS 423
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 176 -----GGKVQRGLIVPHSSSEGSTV----SYDLFDAQQGY 205
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 424 LAKSTSNDNPVVYQYAHARISSLIRSGK-EQGLEVTKDADMSILOTEAEYDLLKVLGEF 482
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 206 PDTLL-----RIYRDNKTINSNLHI 226
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 483 ADVVAEAAAKRAPHRIVRYLNDLASAFHFYNSKNKVLDMONLEV 526
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 48

H71602

protein with DnaJ domain (RESA-like) PFB0920w - malaria parasite (Plasmodium falciparum)

C/Species: Plasmodium falciparum

C/Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004

C/Accession: H71602

R/Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.#
; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998

A/Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.

A/Reference number: A71600; MUID: 99021743; PMID: 9804551

A/Accession: H71602

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-1014 <GAR>

A/Cross-references: UNIPROT:O96276; GB:A5001425; GB:A5001362; NID:G3845310; PIDN:AAC7199

A/Experimental source: clone 3D7

C/Genetics:

A/Gene: PFB0920w

F/677-742/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 7.1%; Score 87.5; DB 2; Length 1014;
Best Local Similarity 23.2%; Pred No. 50;
Matches 52; Conservative 36; Mismatches 79; Indels 57; Gaps 11;

Qy 8 NEKDLRKSE-LQRNALSNLRQIYY-----YNEXAITENKESDDQFLENTLLFKGPF 58
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 204 NGEDIKTMTWLFEMENEKEYLLKGRLYKNNKFMEKYTDE-----YF 252
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 59 TGHPW---YNLLVDLGSKDATNKYKKKVDLYGYGYQCAGTTPNKTACMYGGVTUHDN 116
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 253 PRKWNYNNDLIYK-GSKDLEELKNMFYEWY-----KQEN 287
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 117 NRLTEEKVPINLWDGKQTVPIDKVKTSKEVTVOELD-LQARHYLHGKFGLYNSD-S 174
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 288 LNLEYRRLTVLCRTGWKAL---YNYVENICKETIHSDLDLIIRKNGSNMKGLYNNFYK 344
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 175 FGGKVQRGLIVFHSSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKT 218
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 345 NNGK-----NPPFNTS-SSIDNKKLYNSFGKFNPCFNYESDLSLT 393
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 49

H82177

conserved hypothetical protein VC1606 [imported] - Vibrio cholerae (strain N16961 serogroup conserved)

C/Species: Vibrio cholerae

C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C/Accession: H82177

R/Haidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.#
; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B.;
Chadson, D.; Ermolaeva, J.A.

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: H82177
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-476 <**HBI**>
A;Cross-references: UNIPROT:Q9KRN0; GB:AE004239; GB:AE003852; NID:g9656130; PIDN:AAP947616C
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC1606
A;Map position: 1

Query Match 7.0%; Score 87; DB 2; Length 476;
Best Local Similarity 20.5%; Pred. No. 21;
Matches 52; Conservative 42; Mismatches 94; Indels 66; Gaps 11;

Qy		6 EINEKDRIKKSELORNALSNLROIYYNEKAITENKESDDQFLENILL-----FKGFFT 59
Dd	:	: : : : : : :
Dd	:	: : : : : : :
Dd	:	: : : : : : :
Dd	:	: : : : : : :
Dd	:	: : : : : : :
Dd	:	: : : : : : :
Dd	:	: : : : : : :
Dd	:	: : : : : : :
Dd	:	: : : : : : :
Dd	:	: : : : : : :
Dd	:	: : : : : : :
Dd	:	: : : : : : :
Dd	:	: : : : : : :
Dd	:	: : : : : : :
Dd	:	: : : : : : :
Dd	:	: : : : ~~~~~~PEVLYGDYSEHEDDSL 320
Dd	:	: : : : ~~~~~~BLYLASIR 429
Dd	:	: : : : ~~~~~~EVTVOELD 156
Dd	:	: : : : ~~~~~~DKVKTSKK-
Dd	:	: : : : ~~~~~~WLVGVGNIPLIENSRSRGEQVCANSAVNQRVLAKAQDLSLVEKTY 377
Dd	:	: : : : ~~~~~~SEGSTVSVDLPDAQGYPTLLRIYR 214
Dd	:	: : : : ~~~~~~AQNLRKRKFSGSLTSDVVDA----
Dd	:	: : : : ~~~~~~DNKTINSENHLIDL 228
Dd	:	: : : : ~~~~~~QQSASFNYLISL 443

RESULT 50
AF1489
cell wall-associated protein precursor wpaA (B. subtilis) homolog lin0454 [imported] - Lf
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AF1489
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
. ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Psihi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AP1489
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2167 <**GUA**>
A;Cross-references: UNIPROT:Q92EK5; GB:AL592022; PIDN:CAC95686.1; PID:gl6412895; GSPDB:G
A;Experimental source: strain Clipi1262
C;Genetics:
A;Gene: lin0454

Query Match 7.0%; Score 87; DB 2; Length 2167;
Best Local Similarity 24.0%; Pred. No. 1.4e+02;
Matches 56; Conservative 27; Mismatches 86; Indels 64; Gaps 14;

Qy		30 YYNKEAITENKESDDQFLNTLLPKFGPFTGHPI--WYNDL----LVLDLGSKDATNKY-KG 82
Dd	:	: : : : : : :
Dd	:	: : : : ~~~~~~VAINHGYTAKTSITYNDLDRNRTVNDGSKNAYFEDEF 1729
Dd	:	: : : : ~~~~~~GAYGYQCAGGTNNKTCMYGGVTLHNRLTE---EKKVPINLTWDKG 134
Dd	:	: : : : ~~~~~~KVNVYTAGNGTAANYTDSTQKVNTAAISSAGTGILDENTYDAASNRTSIDNKODQG 1789

Qy	62	PWYNDLLVDLGSKATNKYKGVKVDLYGAYGY	---QCAG-----GTENKTAC	100
Db	371	-----NLYDIYPRSNRNYIQNNINKELVWYGNLSCVMGYTYNIWKHMGVIGPINILY		425
Qy	107	MYGVTLDHNNRLTEEEKVPINLWIDGKQTTVPIDKVKTSKKEV---	TVQELDLQAR---	160
Db	426	IMTGILLTDG-----WID-----YTSKDLDKKIMEINCRFLKQ		461
Qy	161	-----HY-----LHGKFLGYNLSDSGGKVQRGL-----	IVF	186
Db	462	SMIHSEYLMYVFMLLSHYCMSPKMKIAKVKGK--SYNQLSF--	YTRSLPCFTILRYMF	516
Qy	187	HSSEGSTVSVDLFDQAQGYQPTDLLRIYRDNKTNSENLHIDLVLVTT	233	
Db	517	YNGRVKIVPNNLVYDLL-NYESLAHIMMCDGSFVKGGGGLYNLQSF	TT	562
RESULT 54				
AG1749				
glycosidase homolog lin2540 [imported] - <i>Listeria innocua</i> (strain Clip11262)				
C;Species: <i>Listeria innocua</i>				
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004				
C;Accession: AG1749				
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P., D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001				
A;Authors: Krefelt, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournon, ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H. A;Title: Comparative genomics of <i>Listeria</i> species.				
A;Reference number: AB1077; MUID:21537279; PMID:11679669				
A;Accession: AG1749				
A;Status: preliminary				
A;Molecule type: DNA				
A;Residues: 1-1090 <GLA>				
A;Cross-references: UNIPROT:Q928J2; GB:AL592022; PIDN:CAC97767.1; PID:g16415062				
A;Experimental source: strain Clip11262				
C;Genetics:				
A;Gene: lin2540				
Query Match 6.9%; Score 86; DB 2; Length 1090;				
Best Local Similarity 22.5%; Pred. No. 72;				
Matches 47; Conservative 35; Mismatches 61; Indels 66; Gaps 14				
Qy	33	NEKAITENKESDDQFLENTLLFKGFP-----TGHP-----	WY-NDLLVDLGSKDATNKY	80
Db	491	DDNTVYEQRDNDEY---MISQGYSADDGTGAPVYPASQWFGNGILLDFTNKDAVNMW	546	
Qy	81	KGKK-----VDLYGAYYQCGAGTTPNKTCMYGGVTLHDNNRLTEEEKVPINLWID	132	
Db	547	TSQREYLLTDVGID-----GFKTDGG-----EMWGRDITTFNSNGEKQEMR-----	587	
Qy	133	GKQTTVPIDKVKT---SKKEVTVOELDLQARHYLHG--	KFGLYNS-----DSFGGKVQ	180
Db	588	---NRYPTDYSSVPDFPAKSINPEAVSP-SRSGTSGAQSGLIYNSGDQTSFDSFQASVK	643	
Qy	181	RGLIVFHSSEGSTVSY-----DLFDAQGYQY	206	
Db	644	AGL-----SASTSGVSYAWMDMAGFTGNYP	668	

Db 374 LPEDGVQ-----VQMSKRTGKSVTMRDLIEVGLDATRYF---FAMKSSDTHNFDMFS 423
QY 176 -----GGKVQGLIVFHSSEGSTV-----SYDLFDAQQGY 205
Db 424 LAKSTSDNPVYVQYAHARISSILRSKG-EQGLEVSKDANNLSLLETEAEYDLLKVLGEF 482
QY 206 PTLI-----RIYRDNKTINSENLIHI 226
Db 483 ADVAEAAVKRAPIRVIRYLNLDATAFHRFYNSKNVLDMDNLEV 526

RESULT 57
D86342
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 16-Aug-2004
C:Accession: D86342
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D86342
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-614 <STO>
A:Cross-references: GB:AE005172; NID:g4836893; PIDN:AAD30596.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
C:Superfamily: Pyrophosphate-dependent phosphofructokinase, PfpB type; 6-phosphofructoki

Query Match 6.9%; Score 85; DB 2; Length 614;
Best Local Similarity 30.6%; Pred. No. 42;
Matches 26; Conservative 8; Mismatches 35; Indels 16; Gaps 3;
QY 74 KDATNKYKGGKVDLYGAYGYQCAGTGNKTACMYGGV-----LHDNNRLTEE 122
Db 412 KEGT--YKGGKFNACHFFGYQARGSLPSKFCDCYAYVLGHICYHVAAGLNGYMATVTN 469
QY 123 KKPINLWIDGKQTTVPIDKVKTSK 147
Db 470 LKSPVKNK---KCGATPITAMMTVK 491

RESULT 58
T10102
C:Species: Ricinus communis (castor bean)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10102
R:Todd, J.F.; Blakeley, S.D.; Dennis, D.T.
Gene 152, 181-186, 1995
A:Title: Structure of the genes encoding the alpha- and beta-subunits of castor pyrophos
A:Reference number: Z16949; MUID:95137384; PMID:7835697
A:Accession: T10102
A:Status: preliminary; translated from GB/EMBL/DDDBJ
A:Molecule type: DNA
A:Residues: 1-617 <TOD>
A:Cross-references: UNIPROT:Q41140; EMBL:Z32849; NID:g483546; PIDN:CAA83462.1; PID:g4835
C:Genetics:
A:Introns: 30/3; 88/2; 126/1; 151/1; 189/1; 211/3; 239/3; 257/3; 284/3; 316/1; 340/3; 37
C:Superfamily: pyrophosphate-dependent phosphofructokinase, PfpB type; 6-phosphofructoki
C:Keywords: phosphotransferase

Query Match 6.9%; Score 85; DB 2; Length 617;

Best Local Similarity 30.2%; Pred. No. 42;
Matches 26; Conservative 9; Mismatches 35; Indels 16; Gaps 3;
QY 74 KDATNKYKGGKVDLYGAYGYQCAGTGNKTACMYGGV-----LHDNNRLTEE 122
Db 412 KEGT--YKGGKFNACHFFGYQARGSLPSKFCDCYAYVLGHICYHVAAGLNGYMATATN 469
QY 123 KKPINLWIDGKQTTVPIDKVKTSK 148
Db 470 LKNPVKNKRCG---AAPIAAMMTVKR 492

RESULT 59
B44858
C:Species: Lactobacillus paracasei
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: B44858; C44858; A44850
R:Holck, A.; Naes, H.
J. Gen. Microbiol. 138, 1353-1364, 1992
A:Title: Cloning, sequencing and expression of the gene encoding the cell-envelope-associ
A:Reference number: A44859; MUID:92381481; PMID:1512565
A:Accession: B44858
A:Molecule type: DNA
A:Residues: 1-1902 <HOLL>
A:Cross-references: UNIPROT:Q02470; GB:M83946; NID:g149580; PIDN:AAA25248.1; PID:g149582
A:Note: sequence extracted from NCBI backbone (NCBIN:112261, NCBIP:112263)
A:Note: the source is designated as Lactobacillus paracasei subsp. paracasei
A:Accession: C44858
A:Molecule type: protein
A:Residues: 'X', 189-196 <HOL2>
R:Naes, H.; Nissen-Meyer, J.
J. Gen. Microbiol. 138, 313-318, 1992
A:Title: Purification and N-terminal amino acid sequence determination of the cell-wall-l
A:Reference number: A44850; MUID:92226694; PMID:1564442
A:Accession: A44850
A:Status: preliminary
A:Molecule type: protein
A:Residues: 189-196 <NAE>
A:Cross-references: PIDN:AAB22052.1; PID:g248666
A:Experimental source: strain NCDO 151
A:Note: sequence extracted from NCBI backbone (NCBIP:94706)
C:Genetics:
A:Gene: prtP
C:Superfamily: lactocepin; subtilisin homology
C:Keywords: hydrolase; serine proteinase; transmembrane protein
P:1-23/Domain: signal sequence #status predicted <SIG>
F:23-187/Domain: propeptide #status predicted <PRO>
F:188-1902/Product: serine proteinase, cell-envelope-associated #status experimental <NA>
F:208-634/Domain: subtilisin homology #status atypical <SBT>

Query Match 6.9%; Score 85; DB 1; Length 1902;
Best Local Similarity 25.8%; Pred. No. 1.7e+02;
Matches 51; Conservative 12; Mismatches 69; Indels 66; Gaps 8;
QY 46 QFLENTLLFK-----GFFTGHHPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYG 93
Db 805 QFVEGFLNFKGSGSRLNLPYMGFFGD---WND-----GKIVDSLNG-IT 845
QY 94 YOCAGTGNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTQ 153
Db 846 YSPAGGN-----YGTVPLLTNKNTGHQYVGWTDADGKQT----- 881
QY 154 ELDLQARHYLHGKFGLYNSDSFGGKVGQGLIVFHSSEGSTVSVDLPDAQSQYPTLLRIY 213
Db 882 -VDDQIAFSSDKNALYNDISHWYILRNI-----SNVQVILDGGGNKVTLLSS-- 930
QY 214 RDNKTINSENHLIDLYL 231
Db 931 STNQTKTYDAHSQKIY 948

Query Match 6.8%; Score 84; DB 2; Length 227;
Best Local Similarity 21.2%; Pred. No. 15;
Matches 48; Conservative 42; Mismatches 90; Indels 46; Gaps 10;
QY 6 EINEKDLKKSELQNRN---ALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHP 62
DB 34 EYRSQATQDLSEYKGRGFELTNVGYKGNKVTFDNSQQIDVTL-----TG-- 81
QY 63 WYNDLLVDLGSKDQATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLLHNNRLTEE 122
DB 82 --NEKLTWKDDDEVN-----VDVFFVREGSDKSAITTS-----IGGIT-KTNGTQHKD 127
QY 123 KKVPIINLWID---GKOTT-VPIDKVKTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGK 178
DB 128 TVQNVNLSVSKSTGQHTTSVTSEYYSIYKEEISLKLDELFLKRLKHLIDKHDLKYKTEPKDSK 187
QY 179 VORGLIVFHSSEGSTVSVDLPDAQQYPTDLRIYRDNKTINSENL 224
DB 188 IR-----ITMKNGGYVTFEL-----NKKLQPHRMGDTIDSRNI 220
RESULT 64
D86671
transposase of IS1077C [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: D86671
R:Botolin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: D86671
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-272 <STO>
A:Cross-references: UNIPROT:09CII18; GB:AE005176; PID:g12723243; PIDN:AAK04470.1; GSPDB:G
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: tra1077C
Query Match 6.8%; Score 84; DB 2; Length 272;
Best Local Similarity 21.5%; Pred. No. 18;
Matches 42; Conservative 30; Mismatches 67; Indels 56; Gaps 7;
QY 5 BEINEKDLKKSELQNRNLSNRQIYYNEKAITENKESDDQFLENTLLFKGFTGHPWY 64
DB 19 ERVNDKDLLEKEMLK-----IRQ-----EHANAGYRPMRELLKQRGYHVNKKV 62
QY 65 NDLLVDLGSKDQATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLLHNNRLTEEKK 124
DB 63 QRLMKKGLRVTSYWHKSRK-----YNSYKGVGTVAKN-----KLHRRFR----- 103
QY 125 VPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGLI 184
DB 104 -----TSIPHQKITDTTTEPKYEDGKQCYLNPYALFNSE-----VI 143
QY 185 VFH-SSEGSTVSVDL 198
DB 144 SYHISKQPSYQSIDI 158
RESULT 65
F70339
glycerol kinase - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: F70339
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: F70339

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-492 <AQF>
A:Cross-references: UNIPROT:O66746; GB:AE000690; NID:g2983100; PIDN:AAO6710.1; PID:g298;
A:Experimental source: strain VF5
C:Genetics:
A:Gene: gipk
C:Superfamily: xylokinease
Query Match 6.8%; Score 84; DB 2; Length 492;
Best Local Similarity 25.7%; Pred. No. 39;
Matches 61; Conservative 30; Mismatches 74; Indels 72; Gaps 15;
QY 9 EKDLRKKSELQNRNLSNRQ---IYYNEKAITENKESDDQFLENTLLFKGFTGHPWYN 65
DB 44 EQDPLELWEAVRKSLSSEVIQQVGLKEINSIGITNORE-----TVILWDKETGRPVYN 95
QY 66 DLL-VDLGSKDQATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLLHNNRLTEEKK 124
DB 96 AILMODLTEDIC-----RKLSEYSEYIKENT-----GLLLHPYFSASK--- 134
QY 125 VPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGK---FGLYNS-----DSFGK 178
DB 135 --VN-WI-----IENVGVKKDIE-----RGKVFSTVDTWILWNLTGSK 171
QY 179 VORGLIVFHSSEGSTVSVD-LFDAQG-QYPDTLLRIYRDNKTINSE-NLHIDLILYT 232
DB 172 V-----HKTEPSNASRTLLFNIRKLEYDDELLKIFRIPKNILPEVNESLSFGYT 221
RESULT 66
T41863
chitinase chi-A orf126 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
C:Species: Bombyx mori nuclear polyhedrosis virus, BmsNPV
A:Variety: isolate T3
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41863
R:Gomi, S.; Majima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A:Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A:Reference number: Z22020; MUID:99281911; PMID:10355780
A:Accession: T41863
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-552 <KAM>
A:Cross-references: UNIPROT:O92482; EMBL:L33180; NID:g3745835; PIDN:AAC63792.1; PID:g374;
A:Experimental source: isolate T3
C:Superfamily: Serratia marcescens chitinase
Query Match 6.8%; Score 84; DB 2; Length 552;
Best Local Similarity 24.3%; Pred. No. 45;
Matches 45; Conservative 23; Mismatches 69; Indels 48; Gaps 11;
QY 32 YNEKAI---TENKESDDQFLENTLLFKGFTGHPWYNLLVDLGSKDQATNKYKGGKVDLY 88
DB 359 YDKIAVAVYAEAAQSLDKIFLMTYDFK-----AWSN---TDLGYQTTVYAPSWNSELY 410
QY 89 GAYGYQC---AGGTPNKT---ACMYG---GVTLLHDN-NRLTEKKVPIN-LWIDGKQT 136
DB 411 TTHYAVDALLEGVDPNKLIIVGVAMRGWGTGVTYTNNGYSGTGNGPVSCTWEDG--- 467
QY 137 TVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGLIYVPHSSEGSTVS 196
DB 468 -----VDYRQIQKDLNNY-----VYTFDS-----AAQASYVFDKSKGDLISF 505
QY 197 DLFDA 201
DB 506 DSVDS 510
RESULT 67
T44118
penicillin-binding protein 2 [imported] - Staphylococcus aureus

[illegible]

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36595
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36595
A;Molecule type: DNA
A;Residues: 1-507
A;Cross-references: UNIPROT:Q02480; EMBL:X7464; NID:G397068; PIDN:CAA524888
C;Superfamily: papillomavirus L1 protein
C;Keywords: late protein

Query Match	6.7%; Score 83.5; DB 2; Length 507;
Best local Similarity	20.3%; Pred. No. 44;
Matches	Conservative 38; Mismatches 69; Indels 85; Gaps 14
Qy	42 ESDQFLENTLLF-----KGFTHGPWYNDLLVDLGSKD-----ATNKYKGKKVD 86 : : : : : : : : : : : : : : : : : : : Dd QSTDVEYVERTNIFVHAISDRLLTVGHPYY----DVRSGDGORIEVPKVSGNQYRAFRFS 77
Qy	87 -----LYGYAYYGQCAGGTF-----NKTCAMVG 109 : : : : : : : : : : : : : : : : : : :
Dd	78 LPDPNRFPALADMSVYNPKERLVWCARGEIORGQPLGVGTSGHELFENKVRRTSSNNVQ 137
Qy	110 GVTLHDNNRLTBEKKVINLMWDIGQTTPVI-----DKVKTSKKEVTVOELDL---QAR 160 : : : : : : : : : : : : : : : : : : :
Dd	138 GTTMDDRRQNTSFDPK-QVMFTIIG--CIPCLGEHWDRAKVCEKAN-NQLGLCPPIELR 192
Qy	161 HYLHCKFLYNSDSFG---GKVQRGLIVPHSSEGSTVSVDLPDAOGYPDITLLR---IYR 214 : : : : : : : : : : : : : : : : : : :
Dd	193 NIV-----IEDGMFDIGFGNNKELFNKSD---VSLDIVDETCKYPDFLTMANDVYG 244 : : : : : : : : : : : : : : : : : : :
Qy	215 D 215
Dd	245 D 245

RESULT 74
AF1418
ABC transporter, ATP-binding protein homolog lmo2751 [imported] - *Listeria monocytogenes*
C:Species: *Listeria monocytogenes*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AF1418
R:Glaser, F.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Smoes, N.; Tiersz, A.; Varquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AF1418
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-573 <GLA>
A:Cross-references: UNIPROT_Q8Y3T0; GB:NC_003210; PIDN:CAD00964.1; PID:gl6412251; GSPDB:
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo2751

```

Query Match      6.7%; Score 83.5; DB 2; Length 573;
Best Local Similarity 23.3%; Pred. No. 51;
Matches 45; Conservative 30; Mismatches 81; Indels 37; Gaps 8

Qy 22 ALSNLRQI--YYNEKATENKESDDQFLNTLLFKGF---FTGH--PWNOLLVD-----70
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 298 ALISLKRITEVLETPDITYNEAPEQDLGTVFERNVSFKYDGDTPALEDISFKASVG 357

Qy 71 --LGSKDATNKYKKKVDLYGYGYQCAGGTPNKATACWYGVTLHNNRLRTEKKVPIN 128
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 358 EMWGVTVGATGSGKSTLAOLIPRLY-----DPTGEVIIGCTNLKDINKKTLRSTVSFV 410
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::

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Qy 129 LWIDGKQTVTFIDVKVTSKKEVTVQVELD-----LQARHYLHGKFGGLYNS-----DSFGG 177
|      :      :      :      :      :      :      :      :      :      :      :      :      :      :
Db 411 LQAILFSGTTIADNLRHGKKDATAEMEHSKIAQAKEFIDKQAKLYEAPVSESGNFMFSG 470
|      :      :      :      :      :      :      :      :      :      :      :      :      :      :
Qy 178 -----KVQRLGI 184
|      :      :      :      :      :      :      :      :      :      :      :      :      :      :
Db 471 GQKQRLSITRGVI 483
|      :      :      :      :      :      :      :      :      :      :      :      :      :      :

RESULT 75
183350
C:outer membrane usher protein cssD precursor - Escherichia coli
C:Species: Escherichia coli
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: 183350
R:Willshaw, G.A.; Smith, H.R.; McConnell, M.M.; Rowe, B.
FEMS Microbiol. Lett. 49, 473-478, 1988
A:Title: Cloning of genes encoding coli-surface (CS) antigens in enterotoxigen
A:Reference number: f60266
A:Accession: 183350
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-819 <RES>
A:Cross-references: UNIPROT:P53512; EMBL:U04844; NID:g442375; PIDN:AAC45096.1;
C:Superfamily: outer membrane usher protein fimb
C:Keywords: membrane protein

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Query Match	6.7%	Score 83.5;	DB 1;	Length 819;
Best local Similarity	21.4%	Pred. No. 80;		
Matches 54;	Conservative 35;	Mismatches 102;	Indels 61;	Gaps 11
Qy	12	LRKSEL-QRNALSNLRQIYYNKEAITEKNESDDQFLENTLLFKGFFTGHPWYNLLVD	70	
Db	201	LRNREFNQNDKKTWERNYILEKSFYDKK-----LNLVGESYTSNNVNNVSYFTG	253	
Qy	71	LGSKDATTNYGKKGVLDYGYGYQCAGTGNKTKACMYGGVTLHDNNRLTEKKVP----	126	
Db	254	ISVSTDTDMYTPSEIDYTPPEIHG-----VADSDSQIIIVRGNTIIIIINESVPAGPF	303	
Qy	127	----INLWIDGQKTTVPIDRKVTSKKEVTV-----QELDLQARVHLHGK-----	166	
Db	304	SFPITNLMYTGQGLNVEITDVIYGNKKQYTVSNSSLPVNMRKAGLMVYVFIQKLTTKKNSD	363	
Qy	167	-----PGL-YNSDSFGCKVQGLIIVPHSSSEGSTVSVDLFDQAQGYPTDLLRIYRD	215	
Db	364	GDFPAQGDINTGYHYNVTLFGG-YQFSKNYPNLSTG--IGTDL-----GFSGAWLLNVSRS	416	
Qy	216	N-KTINSENLHI	226	
Db	417	NFKDKNGYINIL	428	

RESULT 76
C96884
transposase of IS107F [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)
C/Species: *Lactococcus lactis* subsp. *lactis*
C/Date: 23-Mar-2001 #sequence revision 23-Mar-2001 #text_change 09-Jul-2004
C/Accession: C96884; C96893; H86727
R/Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A/Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ssp.
A/Reference number: A86625; MUID:21235186; PMID:11337471
A/Accession: C96884
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-272 <STO>
A/Cross-references: UNIPROT:O9C806; GI:AE005176; PID:g12725128; PIDN:AAK06173.1; GSPDB:G
A/Experimental source: strain IL1403
A/Accession: C96893
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-272 <ST2>

A;Cross-references: GB:AE005176; PID:g12725206; PIDN:AAK06245.1; GSPDB:GN00146
A;Experimental source: strain IL1403
A;Accession: H86727
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-272 <ST3>
A;Cross-references: GB:AE005176; PID:g12723748; PIDN:AAK04922.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: tral077F; tral077G; tral077E

Query Match 6.7%; Score 83; DB 2; Length 272;
Best Local Similarity 21.5%; Pred. No. 22;
Matches 42; Conservative 30; Mismatches 67; Indels 56; Gaps 7;
QY 5 EBINEKDLKSKSELQNALSNLRQIYYNEKAITENKESDDQFLNLLFKGFTGHWPY 64
DB 19 ERVNDLELEKEMLK-----TRQ-----EHANAGYRPMRELLKQRGVHNVKKV 62
QY 65 NDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMGYGVTLHDNNRLTEKK 124
DB 63 QRLMKKGLRVTSYWHKSRK-----YNSYKGVGTVAKN-----KLHRRFR----- 103
QY 125 VPINLWIDGKQTVPTDKVTSKKEVTVOELDQARHYLHGKFLYNSDSFGKQVORGJI 184
DB 104 -----TSIPHQKITTDTEPKYEDGKQKCYLNPYIDLNSE-----VI 143
QY 185 VFH-SSEGSTVSVDL 198
DB 144 SYHISKQPSYQSIDI 158

RESULT 77
C83996
hypothetical protein BH2771 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: C83996
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83996
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <STO>
A;Cross-references: UNIPROT:Q9K979; GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BA064
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2771

Query Match 6.7%; Score 83; DB 2; Length 379;
Best Local Similarity 29.3%; Pred. No. 34;
Matches 27; Conservative 14; Mismatches 35; Indels 16; Gaps 3;
QY 8 NEKDLKSKSELQNALSNLRQIYYNEKAITENKESDDQFLNLLFKF-----GFFTGHPW 63
DB 107 SEGYRKVARLQKYDRAATQI---NQKADAFERFTSFENTWDYAKNEVAYFTKPM 163
QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYG 95
DB 164 IPDLF-----NVCKGRQVLIVARYAGFE 186

RESULT 78
B83986
hypothetical protein SA1774 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: B83986
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: B89986
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-381 <KUR>
A;Cross-references: UNIPROT:Q99S88; GB:BA000018; PID:g13701758; PIDN:BA043051.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1774

Query Match 6.7%; Score 83; DB 2; Length 381;
Best Local Similarity 22.6%; Pred. No. 34;
Matches 61; Conservative 34; Mismatches 71; Indels 104; Gaps 15;
QY 9 EKDLKSKSELQ-NALSNLRQIYYNEKA-----ITENKESDDQFL-ENTL-LFKGFFT 59
DB 43 ETKLQAKAEAEVSSLPKSAQSLSNQSRFFMDINKNVNKEKLLPETIDRIFEDLTT 102
QY 60 GHPWYNDLLVDLGSKDATNKYKGGK-----VDLYGAYGY-----QCAGGTPNKTACMGYGV 111
DB 103 NHP-----LLADLGIKNAGLRLKFLKSETSGVAVWGKIYGEIKGQDLDAFSEETAI----- 153
QY 112 TLHDNNRLTEKKVPINL-----WID-----GKQTVPTDKVK 144
DB 154 ----QNKLTAFVVLPKDLNDFGPAWIERFVRVQIIEAFAVALETAFLKGTGKQDQIGLNR 209
QY 145 TSKEKVTVOELDQARHYLHGKFLYNSDSFGKQVORGJIVF-----HS 188
DB 210 QVQKGVSVTE-----GAYPE-----KBEQGLTFANPRATVNLTLQVPKYHS 251
QY 189 S-EGSTVSYS-----DLFDAQGOY 205
DB 252 TNEKGSVAVGNVTVMVNPSPDAFEVQAOY 281

RESULT 79
A71509
probable transcription termination factor - Chlamydia trachomatis (serotype D, strain UW:
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
R;Stephens, R.S.; Kallman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tract
A;Reference number: A71570; MUID:9900809; PMID:9784136
A;Accession: A71509
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-464 <ARN>
A;Cross-references: UNIPROT:O84498; GB:AE001322; GB:AE001273; NID:g3328916; PIDN:AAC68091
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: rho
C;Superfamily: transcription termination factor rho
C;Keywords: transcription termination

Query Match 6.7%; Score 83; DB 2; Length 464;
Best Local Similarity 25.7%; Pred. No. 43;
Matches 62; Conservative 23; Mismatches 64; Indels 92; Gaps 14;
QY 1 SEKSEINEKDLKSKSELQNALSNL-----RQIYYNEKAITENK-----ESDDQ 46
DB 37 TEKETSPQVATKTAQLQRMGINELNVLARQYGVNGLSKSQVVFELVAKSERPDE 96
QY 47 FL-ENTL-LFKGF-FTGHPWYN-----DLLV-----DLGSKDA-----TNKYK 81
DB 97 FLIGGVLEVLDPDGFGLRSPTVNYLPSAEDIYVSPAQRRLFKGDTIVGTIRSPKEK 156
QY 82 GK-----KVDLYGAYGYCAGGTPNKT--ACMGYGVTLHDNNRLTEKKVPINLWIDG 133
DB 157 EKYFALLKVD-----KINGSTPDKAKERVLFENLTLHPNERLIME----- 197

Db 468 SSILNOLLAFVWDLSDMG-RESVSRVASIGDRANLYSLLYGKYVTEKTEASVPYG 526

QY 110 GVTLDHNNRLTEKKVPIINLWIDGQTTVPIDKVTSSKEVTVOQLD-----LQARHYLH 164

Db 527 -----FKGHLETHYAVEN-----QYMLPF--VKTADAIYSESELDRLPALAKQAMLK 574

QY 165 GKFGLYNSDSFGKQVORGLIVFHSSEGST-----VSVDLFDAGQYPTDILLRIYR 214

Db 575 G-----IILKDPGKTEQTPKPSNLTITSKITAKAQYQNGLLTWTG 616

QY 215 DN 216

Db 617 EN 618

RESULT 83

E71604

hypothetical protein PF0870w - malaria parasite (Plasmodium falciparum)

C:Species: Plasmodium falciparum

C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004

C:Accession: E71604

R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998

A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.

A:Reference number: A71600; MUID:99021743; PMID:9804551

A:Accession: E71604

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-2380 <GAR>

A:Cross-references: UNIPROT:O96266; GB:AE001421; GB:AE001362; NID:G3845293; PIDN:AACT7196

A:Experimental source: clone 3D7

C:Genetics:

A:Gene: PF0870w

Query Match 6.7%; Score 83; DB 2; Length 2380;

Best Local Similarity 23.1%; Pred. No. 3.4e+02;

Matches 46; Conservative 25; Mismatches 68; Indels 60; Gaps 9;

QY 2 EKSEINEKDLRKKSSELQNALSNLQIYY-----NEKAIT--ENKESDD 45

Db 81 KKNVILNEDDITKNKELVDESFPN---IPFENYFKNLFNLDVSNKNVINIEQKEGDE 137

QY 46 QFLENTLLFKGPTGHPWYNLDLVLGSKDATNKYK-----KKVDLYGAYGYQCAGGTP 101

Db 138 RNADNNLKNKIV-----RDNINKIKTRVNEILLYNNKIINFNDI- 181

QY 102 NKTAC-----MYGGVTILH-----DNNRLTEKKVPIINLWIDGQTTVPIDKVKIT 145

Db 182 --TKKIEIANFISFYFFFLHKKIDLNKNDNGLMKNKSSLK---DICNKKIYKIKIT 236

QY 146 SKKEVTVOQLDQARHYLH 164

Db 237 SKKYISSNDMDTCIRNYL 255

RESULT 84

E71118

uncharacterized protein, ykri B. subtilis homolog [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C:Accession: E71118

R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: E71118

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-247 <KUR>

A:Cross-references: UNIPROT:Q97182; GB:AE001437; PIDN:AAK79736.1; PID:G15024741; GSPDB:G

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC1771

Query Match 6.7%; Score 82.5; DB 2; Length 247;

Best Local Similarity 22.2%; Pred. No. 21;

Matches 52; Conservative 37; Mismatches 90; Indels 55; Gaps 11;

QY 5 BEIN--EKDLRKKSSELQNALSNLQIYYNEKAITENKESDDQFLENTLLFKGPTGHP 62

Db 36 OBINIKSKISTKALRRFALAATAILIF-----FIINSIYGMIFT--- 77

QY 63 WYNDLLVDLGSKDATNKYKGVKVDLYGAYGYQCAGGTPNKTACMYGVVTLHNNRLTEE 122

Db 78 -REYVVVDIN-----PNNKNVAMEIHYNYFGNIILQAAKK-----GVSIVKGRNLKF 127

QY 123 K--KVPINLWI-----DGKQTTVPIDKVTSSKEVTVOQLDQARHYL-HGKFG- 168

Db 128 KATNVVINFTAQNDKFDISGKQNTIVI-TIASSKSINDESIDSSLEHVIKENKINA 186

QY 169 -----LYNSDSFGKQVORGL-----IVFHSSEGSTVSVDLFDAGQYPTDILLRI 212

Db 187 RPMIVLGNIDIDYKSKQVIGIPIDKFIILNKVKNPNPSYKFDLNNKKSIDELINI 240

RESULT 85

B99807

exotoxin 9 [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: B99807

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A99758; MUID:21311952; PMID:11418146

A:Accession: B99807

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-292 <KUR>

A:Cross-references: UNIPROT:Q99WH8; GB:BA000018; PID:G13700315; PIDN:BAB41613.1; GSPDB:G

A:Experimental source: strain N315

C:Genetics:

A:Gene: set9

C:Superfamily: toxic shock syndrome toxin

Query Match 6.7%; Score 82.5; DB 2; Length 292;

Best Local Similarity 20.3%; Pred. No. 27;

Matches 51; Conservative 44; Mismatches 71; Indels 85; Gaps 13;

QY 6 EINE--KDLR-----KKSELQNALN-----NLRQIYYNEKAIT--ENKESDD 45

Db 98 EINPKFKDLRAYYTPSLEFKNEIGILKKTTIRPMNIVPDYFIYKIALVGKDKKYE 157

QY 46 QFLENTLLFKGPTGHPWYNLDLVLGSKDATNKYKGVKVDLYGAYGYQCAGGTPNKT 105

Db 158 GVHRNV-----DVFVLEEK--NKY---GVRYSV----- 182

QY 106 CMYGGVTLHNNRLTEKKVPIINLWIDGQTTV--PIDKVTSSKEVTVOQLDQARHYL 163

Db 183 ---GGITKSNKKV--DHKAGVRITKEDNKGITSHDVSBFKITKEQISLKBELDFLURKQL 237

QY 164 HGKFGLYNSDSFGKQVORGLIVFHSSEGSTVSVDLFDAGQYPTDILLRIYRDKNT----- 218

Db 238 IENHNL-----GNVSGKVIINMKNG-----GKTFELHKKLOENEMADVID 280

QY 219 --INSENHLIDL 228

Db 281 GTNIDNIEVNI 291

RESULT 86

C64716

Db 311 ETDQLLN-----NRAKSKVKL-----VVDGVEIETDLSAT 344
QY 123 KKVPLNLWDGKQTTVPIDK-----VKTSSKEVTQ-----ELDLQARHYLHGKF 167
Db 345 KVA-WRFDEAKYKRIERALKSLBELKEKLAKIEQIEKQNIKILTRKKEWY----- 399
QY 168 GLYNSDSFGGKQVQG--LIVP--HSSEGSTV-----SYDLF---DAQGGVPTDLLRIYR 214
Db 400 -----EKYRWSISRSGYLILGRDASQNESIVKKYLRDKDIFLHADIIGA-PATII-ITQ 452
QY 215 DNKTINSENHL 225
Db 453 DNKTISEEDIY 463

RESULT 90
AH0340
putative autotransporter protein yapC [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH0340
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AH0340
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-638 <KUR>
A:Cross-references: UNIPROT:Q9F290; GB:AL590842; PIDN:CAC93031.1; PID:g15980769; GSPDB:G
A:Genes: yapC

Query Match 6.7%; Score 82.5; DB 2; Length 638;
Best Local Similarity 20.5%; Pred. No. 71;
Matches 43; Conservative 22; Mismatches 64; Indels 81; Gaps 7;
QY 68 LVDLG-----SKDATNKYKGVKVDLYGAYGYQCAGTTPNKTACMYGGVT----- 112
Db 299 VVDLGVYQYGLYSQESNG-----STDWYLATSTELPPTTPNVTAPMLSSAAQGVNLMAA 353
QY 113 -----LHNNRLTEEEKVPINLWDGKQTTV 138
Db 354 APRHILNABELSTLRQGBELKADAETGVGWARYLTDDSRLLSDNKNIAFNILSGNE--I 411
QY 139 PIDKVKTSKEVTQVQELDLQARHYLHGKFLGYNDSFGGKQVQGLIVFHSSSEGSTVSY-- 196
Db 412 GADK-----QLGLNRGNMLIGAFTSYSSSDVKST-----HDANGDIRSYGG 452
QY 197 ----DLFDAGGQVPTDLLRIYRDNKTINSE 222
Db 453 GLYLTLYDQSGFGFYVDTVLKANRFNNKNTQ 482

RESULT 91
AB0122
probable ferric siderophore receptor iutA [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AB0122
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AB0122
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-726 <KUR>

A:Cross-references: UNIPROT:Q8ZHB0; GB:AL590842; PIDN:CAC89837.1; PID:g15979062; GSPDB:G
A:Genetics:
A:Gene: iutA

Query Match 6.7%; Score 82.5; DB 2; Length 726;
Best Local Similarity 25.1%; Pred. No. 83;
Matches 60; Conservative 20; Mismatches 72; Indels 87; Gaps 14;
QY 51 TLLFKGFTGHPWYNLDLVDLGSKDATNKYKGVKVDLYGAYGYQCAGT-----P 101
Db 130 TSLYGGSGTGG-----LINIVTKKG---QEGKQVEL-----QIGGKTGFNSHNDHDE 173
QY 102 NKTACMYGGVTLHDNNRLTEEEKVPINL-----WIDGKQTTVPIDVKVTS---KKEVT 151
Db 174 NISAMSGG-----TERAFGRFSVSYQRYGMYDGKGNVILIDNTQTGLQYSNRUD 224
QY 152 V-----QELDLQARHY---LHGKFGLY-----NSDSFGG 177
Db 225 VMGTGTLNIDENQQLLTQYFNSESDGKHGILGQNSAVTGTGQASNSAALNSDRIPG 284
QY 178 KVQRLIVFHSSEGSTVSYDLFDAGGQVPTDLLRIY-----RDNK--TINSENHLIDLY 229
Db 285 -TERHLINLQYSNTDFWQDQLV-AQVYRDBSLTFYPPPTLKDGVSTIGASQKQTDYF 341

RESULT 92
DB3845
hypothetical protein BH1564 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: DB3845
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: AB83650; MUID:20512582; PMID:11058132
A:Accession: DB3845
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-520 <STO>
A:Cross-references: UNIPROT:Q9KCK7; GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BA052
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1564

Query Match 6.6%; Score 82; DB 2; Length 520;
Best Local Similarity 27.5%; Pred. No. 60;
Matches 46; Conservative 23; Mismatches 58; Indels 40; Gaps 11;
QY 48 LENTLLFKGFTGHP-----WTN---DLLVDLGSKDAT-----NKYK 81
Db 85 IESTLITGSLPDEHKVPVGLVWYHAEEDRLVDYGSTPETYMKLGLNRLVFLDLSLNNRHL 144
QY 82 GKKV-DLYGAYGYQCAGTTPNKTACMYGGVTLHDNNRLTEEEKVPINLWDGK--QTTV 138
Db 145 SKDVPPTIHEILDQSQMSSTGVN--ALVYRGNTSHKVN-LPE-----PFDWMQGPPTKG 197
QY 139 P-IDKVKTSKEVTQVQELDLQARHYLHGKFLGYNDSFGGKQVQGLI 184
Db 198 PLLSGFTIIEPKVIQAKELDDHFL-DLYGL--NDSYGTAVVRTLI 241

RESULT 93
S55243
ubiquitin-like protein 8 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2004
C:Accession: S55243; S61068
R:Callis, J.; Carpenter, T.; Sun, C.W.; Vierstra, R.D.
Genetics 139, 921-939, 1995
A:Title: Structure and evolution of genes encoding polyubiquitin and ubiquitin-like prote
A:Reference number: S55242; MUID:95229071; PMID:7713442
A:Accession: S55243
A:Status: nucleic acid sequence not shown

A:Molecule type: DNA
A:Residues: 1-631 <CAL>
A:Cross-references: UNIPROT:Q39256; EMBL:L05917
A:Experimental source: ecotype Columbia
R:Callie, J.; Carpenter, T.; Sun, C.W.; Vierstra, R.D.
submitted to the EMBL Data Library, June 1995
A:Reference number: S61068
A:Accession: S61068
A:Molecule type: DNA
A:Residues: 1-341, 'E', 343-631 <CAW>
A:Cross-references: EMBL:L05917; NID:g870793; PIDN:AAA68879.1; PID:g870794
C:Superfamily: ubiquitin homology
F:3-78/Domain: ubiquitin homology <UBH1>
F:79-154/Domain: ubiquitin homology <UBH2>
F:155-237/Domain: ubiquitin homology <UBH3>
F:238-318/Domain: ubiquitin homology <UBH4>
F:319-392/Domain: ubiquitin homology <UBH5>
F:393-468/Domain: ubiquitin homology <UBH6>
F:469-551/Domain: ubiquitin homology <UBH7>
F:552-627/Domain: ubiquitin homology <UBH8>
Query Match 6.6%; Score 82; DB 2; Length 631;
Best Local Similarity 21.0%; Pred. No. 77;
Matches 64; Conservative 47; Mismatches 102; Indels 92; Gaps 17;
Qy 2 EKSEINEKDLRKSELOQNALSLNRQIYYNEKAITE-NKESDDQFLEN-----TLIF 54
Db 177 ESSDTI--ENVKAKIQDEGLRPHQRLLIFGEELFTEDNRLADYGINRSTLCIALRL 234
Qy 55 KG-----FFTGHPWYNLLVDLGSKDATNKYKG-----KVDLYGAYY-GY 94
Db 235 RGDVYFVKNLPYNSFTG----ENFILESSDTIDNVKAKLQDKERIPMDLHRLIFAGK 290
Qy 95 QCAGGTNKTACMGV---GVTLHNNR-----LTEEKVPINLWIDGKQTTVP 140
Db 291 PLEGG---RTLAHYNIQKSTLYLTPRCGMQIFVKTLTRK---INLEVESWDT--I 341
Qy 141 DKVKTS-----KKEVTVQELDLQARHYLHGKFL-YNSDSFG 176
Db 342 DNVKAMVDKEGIQPNQLRLIFLGKELKDGCTLADYSIQKSTLHLVLGMQIFVKLFG 401
Qy 177 GKVGRLIVFHSRGSTVSYDLFDAQGYPTLLRIYR-----DNKTY-----NSENLH 225
Db 402 GKIIIT-LEVLSSDTIKSVKAKIQKVGSPPPQQLFRGGQLQDGRITLGDYINIRNESTLH 460
Qy 226 IDLYL 230
Db 461 LFFHI 465
RESULT 94
T05829
hypothetical protein T5K18.240 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 09-Jul-2004
A:Accession: T05829
R:Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Voickaert, G.; Ba
submitted to the Protein Sequence Database, April 1998
A:Reference number: Z15453
A:Accession: T05829
A:Molecule type: DNA
A:Residues: 1-756 <BEV>
A:Cross-references: UNIPROT:O49464; EMBL:AL022580
A:Experimental source: cultivar Columbia; BAC clone T5K18
C:Genetics:
A:Map position: 4
A:Introns: 494/1
A:Note: T5K18.240
Query Match 6.6%; Score 82; DB 2; Length 756;
Best Local Similarity 22.8%; Pred. No. 96;
Matches 66; Conservative 28; Mismatches 96; Indels 100; Gaps 11;

Qy 26 LRQIYYNEK-----AITENKESDDQFL-----ENT----- 51
Db 289 LRQVYQIPEKRVHVLGVNDENGFTSDKLRTLFRSKLGPENSAIVLGAAGRLVKDKG 348
Qy 52 --LLFKGFFTGHPWYNLLVDLGSKDATNKYK--GKKVDLYGAYYGYQCAGGTPNKTAC 106
Db 349 HPLLFEAFAKIIQIYNSVYLWVAGSPWEQRYKELGKVSILGSL-----NPNELKG 400
Qy 107 MYGGVTLHDNNRLTEE-----KKVPINLWIDGKQTTV-----PIDKV 143
Db 401 FYNGIDLVFNPTLRPOGLDITLMEAMLSGKPVWASIRKTIIVNDEFGFMFAPNVEA 460
Qy 144 KTSKKEVTVOE---LDLQARHYLHGKFLYNSDSFGKQVQGL----- 183
Db 461 LTAVWEVAVAEGERLAERGR-----KCEYAAEMFTAKSLRTLQLGSSSTFFKIPTWEK 515
Qy 184 -----IVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHLIDL 228
Db 516 DNVLYLVSHSSCDGLVCLYNHDKSGYVYVNPTRWYRPLPLCDYQKLMIDL 565
RESULT 95
T28156
DNA-directed RNA polymerase homolog - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28156
R:Fox, B.A.; Li, W.B.; Tanaka, M.; Inselburg, J.; Bzik, D.J.
Mol. Biochem. Parasitol. 61, 37-48, 1993
A:Title: Molecular characterization of the largest subunit of plasmodium falciparum RNA I
A:Reference number: Z20478; MUID:94081864; PMID:8259131
A:Accession: T28156
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2910 <FOX>
A:Cross-references: UNIPROT:Q26008; EMBL:L11172; NID:g414321; PID:g414322; PIDN:AAA72349
C:Genetics:
A:Introns: 2840/3; 2880/1
Query Match 6.6%; Score 82; DB 2; Length 2910;
Best Local Similarity 19.7%; Pred. No. 5.2e+02;
Matches 64; Conservative 44; Mismatches 83; Indels 134; Gaps 18;
Qy 2 EKSEINEKDLRKSELOQNALSLNRQIYYNEKAITE-NKESDD-----QFLENTLIF- 54
Db 1382 EKKEKEKE-----NKIANTCINYNKSHVDEQNCNSSLSCYQVYVNLKOLF 1432
Qy 55 --KGFFTG-----HPWYNLLVDLGSKD-----ATNK-YK----- 81
Db 1433 LYEKYLNGKNEEGNKHILYNNQCIDERNDPLNSVTNKLKALKEPTFFNSTSTFKKIT 1492
Qy 82 -----GKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLH----- 114
Db 1493 KVIEKVLITFLAARCNRLKIYIFELFQ-----NKNIMKYFSLVYINIFHFDVSN 1546
Qy 115 -----DNNRLTEKKVPI-----NLWIDGKQTT-----VPIDKVKTS 146
Db 1547 EIKKVNINNIYFKEDESPSISNNNNNNKVEDDCNQDIKIKGQETNEFIDDEKIKTK 1606
Qy 147 KK-----EVTVOEL-DLQARHYLHGKFLYNSDSFGKQVQGLIVFHSSEGSTVSYDLFDAQ 202
Db 1607 RKCSQEKTIQEIKKYKLLKFLHFAELHKKQNY-----BEGR--GYDI-DEQ 1650
Qy 203 GQY---PDTLLRIYRDNKTINSEN 224
Db 1651 NDYNIDEKFMNDYNNNN--NNDNL 1674
RESULT 96
T31076
tyrocidine synthetase 3 - Brevibacillus brevis
C:Species: Brevibacillus brevis
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 04-Apr-2004

C:Accession: T31076
R:Mootz, H.D.; Marahiel, M.A.
J. Bacteriol. 179, 6843-6850, 1997
A:Title: The tyrocidine biosynthesis operon of *Bacillus brevis*: Complete nucleotide sequence
A:Reference number: Z20969; MUID:98012987; PMID:9352938
A:Accession: T31076
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6486 <MOO>
A:Cross-references: EMBL:AF004835; NID:g2623770; PID:g2623773; PIDN:AAC45930.1
C:Genetics:
A:Gene: tycc
C:Function:
A:Pathway: tyrocidine biosynthesis
C:Keywords: carrier protein; phosphopantetheine; phosphoprotein
P:510-950/Domain: acetate-CoA ligase homology <AC11>
P:968-1036/Domain: acyl carrier protein homology <ACP1>
P:1546-1987/Domain: acetate-CoA ligase homology <AC12>
P:2005-2073/Domain: acyl carrier protein homology <ACP2>
P:2583-3025/Domain: acetate-CoA ligase homology <AC13>
P:3043-3111/Domain: acyl carrier protein homology <ACP3>
P:3621-4060/Domain: acetate-CoA ligase homology <AC14>
P:4078-4146/Domain: acyl carrier protein homology <ACP4>
P:4656-5104/Domain: acetate-CoA ligase homology <AC15>
P:5122-5190/Domain: acyl carrier protein homology <ACP5>
P:5702-6147/Domain: acetate-CoA ligase homology <AC16>
P:6165-6233/Domain: acyl carrier protein homology <ACP6>
P:1000,2037,3075,4110,5154,6197/Binding site: phosphopantetheine (Ser) (covalent) #status

Query Match .66%; Score 82; DB 2; Length 6486;
Best Local Similarity 20.2%; Pred. No. 1.4e+03;
Matches 50; Conservative 43; Mismatches 79; Indels 76; Gaps 12;
QY 16 SELOALNSLRQIY-----YNEKAITENKESDDQFLENTLLPKGFPTGH--PMY 64
DB 789 ASMQPVPVGSIGEMYIAGDVAKGYFNRELPETKEFIDNPFPGTKMYR---TGDLAKWL 845
QY 65 NDLLVD-LGSKDATNKYKGVLDLYGAYGYQCAGGTENKTKACMYGGVTLHDNNRLTEEK 123
DB 846 PGNMEYAGRMQYQVKIRHTEM-----GEI-----ETRLTQHE 880
QY 124 KVPINLWIDGKQTTVPIDKVKT-----SKKEVTVOELDQARHYLHGKFGLYNSD 173
DB 881 AV-----KEAVIVKEDSQNVLYAYVLSERELTVAEI-----REFLGRTPSYMP 928
QY 174 SP-----GGKVGRLIVFHSSEGSTSVSYDLFDA-QGYPPDLLRIYRDNKTINS 221
DB 929 SPFFIRLAETPLTANGKVERKKL--PKPAGAVVTGTAYAAPQNEIEAKLAEIWOQVLGISQ 986
QY 222 ENLHIDLY 229
DB 987 VGIHDDFF 994

RESULT 97
A89807
exotoxin 8 [imported] - *Staphylococcus aureus* (strain N315)
C:Species: *Staphylococcus aureus*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A89807
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizukami-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: A89807
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-356 <KUR>
A:Cross-references: UNIPROT:Q99WH9; GB:BA000018; PID:g13700314; PIDN:BAB41612.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:

A:Gene: set8

Query Match .66%; Score 81.5; DB 2; Length 356;
Best Local Similarity 20.0%; Pred. No. 41;
Matches 27; Conservative 31; Mismatches 48; Indels 29; Gaps 3;

QY 64 YNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTENKTKACMYGGVTLHDNNRLTEEK 123
DB 225 YNDIDVFIVLEDD--NKYQLKKYSV-----GGITKTNKKVVDHKA 261
QY 124 KVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVGQRL 183
DB 262 ELSVTYKDNQGMISRDVSEYMITKEEISLSEKELDFKLRLQLEKHNLY-----GNMGSGT 315
QY 184 IVFHSSEGSTSVSYDL 198
DB 316 IVIKMNGGKVTPEL 330

RESULT 98

A40457
replication protein A1 - human
N:Alternate names: replication protein A 70K chain
C:Species: *Homo sapiens* (man)
C:Date: 28-Feb-1992 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
C:Accession: A40457; A44501
R:Erdile, L.F.; Heyer, W.D.; Kolodner, R.; Kelly, T.J.
J. Biol. Chem. 266, 12090-12098, 1991
A:Title: Characterization of a cDNA encoding the 70-kDa single-stranded DNA-binding subunit
A:Reference number: A40457; MUID:91268092; PMID:2050703
A:Accession: A40457
A:Molecule type: mRNA
A:Residues: 1-216, 'A', 218-616 <ERD>
A:Cross-references: UNIPROT:P27694; GB:M63488
A:Note: parts of the sequence determined by protein sequencing
A:Note: this sequence has been corrected in reference A44501
R:Erdile, L.F.; Heyer, W.D.; Kolodner, R.; Kelly, T.J.
J. Biol. Chem. 268, 2268, 1993
A:Title: Characterization of a cDNA encoding the 70-kDa single-stranded DNA-binding subunit
A:Reference number: A44501; MUID:93131993; PMID:8420996
A:Accession: A44501
A:Molecule type: mRNA
A:Residues: 217 <ER2>
A:Cross-references: GB:M63488
A:Note: sequence correction
C:Genetics:
A:Gene: GDB:RPAL
A:Cross-references: GDB:138362; OMIM:179835
A:Map position: 17p13.3-17p13.3
C:Complex: Replication protein A is a trimer of 70K (A1), 32K (A2), and 14K (A3) chains.
C:Function:
A:Description: probable eukaryotic equivalent of prokaryotic single-stranded DNA-binding
probably also has a role in the elongation stage of DNA replication
A:Pathway: DNA replication initiation
A:Note: the single-stranded DNA-binding activity resides in the A1 protein
C:Superfamily: replication protein A1
C:Keywords: DNA replication initiation; single-stranded DNA binding; trimer; zinc finger
F:481-503/Region: zinc finger CCCC motif

Query Match .66%; Score 81.5; DB 1; Length 616;
Best Local Similarity 25.1%; Pred. No. 82;
Matches 56; Conservative 25; Mismatches 57; Indels 85; Gaps 15;

QY 23 LSNLRQIYVY-----NEKAITENKES-----DDQFLENTLLPKGFPTG 60
DB 248 LIEVAKVYFSGTKLKIANKQFTAVKNYEMTFNNETSNVMPCEDDHLP-TVQFD--FTG 304
QY 61 HPWYNDLLVGLSKDATNKYKGVLDLYGAYGYQCAGGTENKTKACMYGGVTLHDNNRLT 120
DB 305 -----ID-----DLENKSKSLVDIIIGICKSYEDA-----TKITVRSNNREV 341
QY 121 EEKKVPINLWIDGKQTTVP-----DKVTSKKEVTVOELDQARHYLHGKFGLYNSDSF 175

Db 342 AKRNIYL-MDTSGKVVTATLWGEDADKPDGSRQRPVLAIK-----GARVSD-F 386
Qy 176 GKGQVQGLIVFHSSEGSTV-----SYDL---FDAQGQYPD 207
Db 387 GG---RSLSVLSS---STIIANPDIPKAYKURGFWDAGQALD 423
RESULT 99
G90571
hypothetical protein MYPU 4790 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: G90571
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissou, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: G90571
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-804 <KUR>
A:Cross-references: UNIPROT:Q98087; GB:AL445566; PID:gl4089893; PIDN:CAC13652.1; GSPDB:C
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPU 4790
A:Genetic code: SGC3
Query Match 6.6%; Score 81.5; DB 2; Length 804;
Best Local Similarity 18.5%; Pred. No. 1.1e+02;
Matches 47; Conservative 42; Mismatches 74; Indels 91; Gaps 9;
Qy 3 KSEINEKDLRKKSGLQNALSNLR-----QIYYNEKA-----ITENKE 42
Db 501 KNYEQDNKDRIKISDDKLYNKIDIRFLLEQWAKTKKIFYGNIEKEINNWLKPFIDQNFK 560
Qy 43 SDDQFLENTLLFKGFTTGHWPYNLDLVLGSKDATNKYK----- 81
Db 561 KD-----ENISIDFGWYVLFKDFKQKQKEIENKLEKNEYKEVVEYQIPRSKNLPFYSEIF 616
Qy 82 ----GKKVDLYGAYGYQCAGGTENKTKACMYGGVTLHDNNRLTEKKVPINLWIDGKQTT 137
Db 617 LEKSNKIDFDNAKNYVE-----QITTKDKNQKDD-----IQLESNET 658
Qy 138 VPIDKVTSTKKEVTQELDLQARHYLGKFLYNSDSFGGKVQVQGLIVFHSSEGSTVSYD 197
Db 659 SFLEEIKRIFKQKHKEIENKNIPIHQ--GI-----GFDYIHNDKHT---- 700
Qy 198 LFDAQGOYVPTLLR 211
Db 701 -----SPPDFIIR 708
RESULT 100
G88637
protein F53H1.4 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G88637
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: G88637
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1378 <STO>
A:Cross-references: UNIPROT:Q45075; GB:chr_IV; PIDN:AAC02578.1; PID:g2854159; GSPDB:GN00
C:Genetics:
A:Gene: F53H1.4
A:Map position: 4

Query Match 6.6%; Score 81.5; DB 2; Length 1378;
Best Local Similarity 20.1%; Pred. No. 2.2e+02;
Matches 54; Conservative 41; Mismatches 100; Indels 73; Gaps 11;
Qy 2 EKSEINEKDLRKKSGLQNALSNLRQIYYNEKAI--TENKESD-----DQFLENTLLFK 55
Db 253 KQKQEQBEKQKKEEKAKKLKEKEEKLKEKEEKAARKAKEKEKNGNGTMDKFLKKD----- 308
Qy 56 GFFTGHF-----WYNDLLVLGSKDATNKYKGVLDLYGAYGYQCAGGTENK 103
Db 309 ---TGSFSSKNAPLFSFSKW-GEKRIAGVKKMEDAWKRRDLEY-----N 350
Qy 104 TACMYGGVTLHDNNRLTEEK---KVPINLWIDGKQTTVPIDKVTSTKKEVTQVQELDLQAR 160
Db 351 EACSWCEKNLSGNQKSTFENPIFKFSYQKLVDAKADRAHMKGMKWAQKAEFKAEWS-EKR 409
Qy 161 HYLHCKF-----GLYNSDSFGGKVQVQGLIVFHSSEGSTVSYDLFDAQ----- 202
Db 410 KELYQKFEPIKAKWFNED-----IALDDLLVTCENLELLELDKRVNCDDELLKCLE 459
Qy 203 -GOYVPTLLRIYRDNKTINGENLHIDLY 229
Db 460 ISQFFVSMRKILLWNENITAEQLRDDLLH 487
Search completed: July 26, 2005, 11:08:47
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 10:59:53 ; Search time 173 Seconds
(without alignments)
689,679 Million cell updates/sec

Title: US-09-900-766-7
Perfect score: 1238
Sequence: 1 SEKSEINKEKLRKKSELR.....RDNKTINSEMLIDLYLTT 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1238	100.0	257	1	ETXG_STPAU
2	1023	82.6	257	1	ETXG_STPAU
3	1023	82.6	257	2	O6G7Y7
4	1023	82.6	257	2	O6G7Y7
5	994	80.3	257	2	O6G7Y7
6	994	80.3	257	2	O6G7Y7
7	971	78.4	257	2	O6G7Y7
8	837	67.6	257	2	O6G7Y7
9	830	67.0	257	2	O6G7Y7
10	825	66.6	257	2	O6G7Y7
11	663	53.6	257	2	O6G7Y7
12	496	40.1	257	2	O6G7Y7
13	490.5	39.6	257	2	O6G7Y7
14	490.5	39.6	257	2	O6G7Y7
15	461.5	37.3	257	2	O6G7Y7
16	461.5	37.3	257	2	O6G7Y7
17	461.5	37.3	257	2	O6G7Y7
18	446.5	36.1	257	2	O6G7Y7
19	446.5	36.1	257	2	O6G7Y7
20	414	33.4	257	2	O6G7Y7
21	387.5	31.3	257	2	O6G7Y7
22	387.5	31.3	257	2	O6G7Y7
23	387.5	31.3	257	2	O6G7Y7
24	381	30.8	257	2	O6G7Y7
25	366	29.6	257	2	O6G7Y7
26	366	29.6	257	2	O6G7Y7
27	366	29.6	257	2	O6G7Y7
28	348.5	28.2	257	2	O6G7Y7
29	348.5	28.2	257	2	O6G7Y7
30	348.5	28.2	257	2	O6G7Y7
31	341.5	27.6	257	2	O6G7Y7

32	339.5	27.4	242	2	O85383
33	339.5	27.4	242	2	O7A2Q5
34	339.5	27.4	242	2	O7A4M8
35	337	27.2	240	2	O7A2N9
36	337	27.2	240	2	O7A4K9
37	337	27.2	240	2	O9F0L7
38	336	27.1	240	2	O8NXJ5
39	335.5	27.1	218	2	O8RR75
40	335.5	27.1	225	2	O9L9Z1
41	334.5	27.0	225	2	O99Z21
42	320	25.8	239	2	O99T47
43	320	25.8	239	2	O7A4W7
44	319.5	25.8	242	2	O8NVM3
45	319.5	25.8	242	2	O6G7U1
46	318.5	25.7	256	2	O8VLM7
47	316.5	25.6	242	2	O93CC6
48	316	25.5	239	2	O9EZM7
49	312	25.2	86	2	O7L1S9
50	310	25.0	242	2	O8NVM2
51	310	25.0	242	2	O6G7U0
52	309	25.0	163	2	O6R2F8
53	309	25.0	242	2	O54476
54	309	25.0	242	2	O93CC5
55	302	24.4	239	2	O6GFM8
56	300.5	24.3	266	1	ETXG_STPAU
57	298	24.1	261	2	O6G7U0
58	298	24.1	261	2	O6G7U0
59	295.5	23.9	251	1	SPER_STRP8
60	295.5	23.9	251	1	SPER_STRP8
61	295	23.8	177	2	O6R1Y7
62	294.5	23.8	251	2	O8K6K5
63	291.5	23.5	261	2	O6XXM3
64	290.5	23.5	261	2	O6XXM5
65	289.5	23.4	207	2	O7XOE8
66	288.5	23.3	261	2	O6XXM4
67	287.5	23.2	218	2	O7XOE7
68	286.5	23.1	239	2	O6G531
69	285.5	23.1	239	2	O6G532
70	285.5	23.1	239	2	O6G532
71	285.5	23.1	266	1	ETXG_STPAU
72	284.5	23.0	239	2	O06535
73	283.5	22.9	239	2	O05157
74	283.5	22.9	239	2	O8NXJ6
75	282.5	22.8	266	2	O06533
76	281.5	22.7	266	1	ETXG_STPAU
77	280.5	22.7	207	2	O7XOE6
78	280.5	22.7	222	2	O6XZB6
79	280.5	22.7	239	2	O6G7Y9
80	279.5	22.6	236	2	O54696
81	279.5	22.6	271	2	O9F0L6
82	278.5	22.5	236	2	O53678
83	278.5	22.5	239	2	O53678
84	277.5	22.4	222	2	O938P4
85	277.5	22.4	222	2	O9S524
86	277.5	22.4	234	2	O9R5X4
87	277.5	22.4	234	2	O54779
88	276.5	22.3	222	2	O9R931
89	276.5	22.3	226	2	O57453
90	272.5	22.0	239	2	O06534
91	269.5	21.8	260	2	O54971
92	267.5	21.6	260	2	O54738
93	267.5	21.6	260	2	O79X14
94	267.5	21.6	260	2	O54739
95	266.5	21.5	266	1	ETXG_STPAU
96	264.5	21.4	258	2	O6GFM2
97	262.5	21.2	222	2	O6XZB7
98	259.5	21.0	254	2	O764P6
99	256.5	20.7	209	2	O9RQO5
100	255	20.7	233	2	O8R777
101	255.5	20.6	233	2	O8R777
102	255.5	20.6	258	1	ETXG_STPAU
103	255.5	20.6	258	2	O9EZM3
104	253	20.4	209	2	O9LAD8

O85383	staphylococ
O7A2Q5	staphylococ
O7A4M8	staphylococ
O7A2N9	staphylococ
O7A4K9	staphylococ
O9F0L7	staphylococ
O8NXJ5	staphylococ
O8RR75	staphylococ
O9L9Z1	staphylococ
O99Z21	staphylococ
O99T47	staphylococ
O7A4W7	staphylococ
O8NVM3	staphylococ
O6G7U1	staphylococ
O8VLM7	staphylococ
O93CC6	staphylococ
O9EZM7	staphylococ
O7L1S9	staphylococ
O8NVM2	staphylococ
O6G7U0	staphylococ
O6R2F8	staphylococ
O54476	staphylococ
O93CC5	staphylococ
O6GFM8	staphylococ
ETXG_STPAU	staphylococ
O6G7U0	staphylococ
O6G7U0	staphylococ
SPER_STRP8	staphylococ
SPER_STRP8	staphylococ
O6R1Y7	staphylococ
O8K6K5	staphylococ
O6XXM3	staphylococ
O6XXM5	staphylococ
O7XOE8	staphylococ
O6XXM4	staphylococ
O7XOE7	staphylococ
O6G531	staphylococ
O6G532	staphylococ
O6G532	staphylococ
ETXG_STPAU	staphylococ
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O06533	staphylococ
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O7XOE6	staphylococ
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O9F0L6	staphylococ
P97163	staphylococ
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O938P4	staphylococ
O9S524	staphylococ
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O9R931	staphylococ
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O06534	staphylococ
O54971	staphylococ
O54738	staphylococ
O79X14	staphylococ
O54739	staphylococ
P01552	staphylococ
O6GFM2	staphylococ
O9ZNF2	staphylococ
O6XZB7	staphylococ
O764P6	staphylococ
O9RQO5	staphylococ
O8R777	staphylococ
O85383	staphylococ
O9EZM3	staphylococ
O9LAD8	staphylococ

105	253	20.4	209	2	Q91AE0	Q91AE0 streptococc
106	251.5	20.3	259	2	Q76LS8	Q76LS8 staphylococ
107	251	20.3	209	2	Q91AC6	Q91AC6 streptococc
108	251	20.3	209	2	Q91AD1	Q91AD1 streptococc
109	249	20.1	209	2	Q91AC4	Q91AC4 streptococc
110	249	20.1	209	2	Q91AE1	Q91AE1 streptococc
111	249	20.1	233	2	Q76M7	Q76M7 streptococc
112	247.5	20.0	220	2	Q79A00	Q79A00 streptococc
113	247	20.0	209	2	Q91AC5	Q91AC5 streptococc
114	246	19.9	209	2	Q91AC7	Q91AC7 streptococc
115	245.5	19.8	159	2	Q6R2G1	Q6R2G1 staphylococ
116	245.5	19.8	214	2	Q6R2E8	Q6R2E8 streptococc
117	244	19.7	209	2	Q91AD2	Q91AD2 streptococc
118	244	19.7	209	2	Q91AD6	Q91AD6 streptococc
119	243	19.6	207	2	Q7MY99	Q7MY99 streptococc
120	243	19.6	233	2	Q6VB17	Q6VB17 streptococc
121	242	19.5	209	2	Q91AD9	Q91AD9 streptococc
122	242	19.5	233	2	Q8N289	Q8N289 streptococc
123	241	19.5	209	2	Q91AC9	Q91AC9 streptococc
124	240	19.4	209	2	Q91AD3	Q91AD3 streptococc
125	239	19.3	209	2	Q91AC3	Q91AC3 streptococc
126	239	19.3	209	2	Q91AC8	Q91AC8 streptococc
127	238	19.2	256	2	Q9S1H8	Q9S1H8 streptococc
128	237.5	19.2	180	2	Q6DTL6	Q6DTL6 streptococc
129	237	19.1	209	2	Q91AD5	Q91AD5 streptococc
130	234	18.9	209	2	Q91AD7	Q91AD7 streptococc
131	233	18.8	209	2	Q91AD3	Q91AD3 streptococc
132	232	18.7	233	2	Q99XW1	Q99XW1 streptococc
133	231.5	18.7	180	2	Q6DTL4	Q6DTL4 streptococc
134	231	18.7	209	2	Q91AD0	Q91AD0 streptococc
135	228	18.4	259	2	Q6DTL3	Q6DTL3 streptococc
136	227	18.3	183	2	Q936G4	Q936G4 staphylococ
137	224	18.1	183	2	Q6DTL5	Q6DTL5 streptococc
138	220.5	17.8	131	2	Q7CEP2	Q7CEP2 streptococc
139	220	17.8	234	2	Q8K807	Q8K807 streptococc
140	218	17.6	183	2	Q6DTL1	Q6DTL1 streptococc
141	217	17.5	234	1	SEBG_STRPY	SEBG_STRPY
142	217	17.5	240	2	Q8P2R5	Q8P2R5 streptococc
143	216	17.4	210	2	Q9K2G9	Q9K2G9 streptococc
144	214	17.3	234	2	Q76FM2	Q76FM2 streptococc
145	213	17.2	234	2	Q76FM3	Q76FM3 streptococc
146	208	16.8	234	2	Q76FNO	Q76FNO streptococc
147	205	16.6	234	2	Q76FM5	Q76FM5 streptococc
148	203	16.4	234	2	Q76FM7	Q76FM7 streptococc
149	201	16.2	157	2	Q99TP7	Q99TP7 staphylococ
150	201	16.2	157	2	Q7AS47	Q7AS47 staphylococ
151	199	16.1	234	2	Q76FM8	Q76FM8 streptococc
152	199	16.1	236	2	Q9L920	Q9L920 streptococc
153	198	16.0	234	2	Q76FM9	Q76FM9 streptococc
154	197	15.9	136	2	Q99T49	Q99T49 staphylococ
155	197	15.9	136	2	Q7A4X0	Q7A4X0 staphylococ
156	197	15.9	195	2	Q6YCN2	Q6YCN2 staphylococ
157	197	15.9	234	2	Q93RR9	Q93RR9 streptococc
158	197	15.9	234	2	Q8G9K7	Q8G9K7 streptococc
159	197	15.9	236	1	SEBH_STRPY	SEBH_STRPY
160	193	15.6	232	2	Q7BAE3	Q7BAE3 streptococc
161	187	15.1	256	2	Q9S1H9	Q9S1H9 streptococc
162	187	15.1	256	2	Q9X9R8	Q9X9R8 streptococc
163	185	14.9	235	2	Q8NKK2	Q8NKK2 streptococc
164	180	14.5	235	1	SEPC_STRPY	SEPC_STRPY
165	168	13.6	206	2	Q6LDJ6	Q6LDJ6 streptococc
166	163	13.2	206	2	Q54512	Q54512 streptococc
167	160.5	13.0	108	2	Q9EZM5	Q9EZM5 staphylococ
168	147	11.9	167	2	Q7X0E4	Q7X0E4 staphylococ
169	144	11.6	62	2	Q99TP8	Q99TP8 staphylococ
170	144	11.6	62	2	Q7A5A8	Q7A5A8 staphylococ
171	138	11.1	167	2	Q7X0E5	Q7X0E5 staphylococ
172	135	10.9	259	2	Q70EW3	Q70EW3 streptococc
173	135	10.8	262	2	Q8P0S0	Q8P0S0 streptococc
174	134	10.8	227	2	Q849U3	Q849U3 streptococc
175	134	10.8	262	2	Q70EW2	Q70EW2 streptococc
176	133	10.7	167	2	Q7MS59	Q7MS59 staphylococ
177	130	10.5	259	2	Q938J1	Q938J1 temperature p

ALIGNMENTS

```

RESULT 1
ID      EXTX STRAU      STANDARD      PRT;      257 AA.
AC      P12993;
DT      01-JAN-1990 (Rel. 13, Created)
DT      01-JAN-1990 (Rel. 13, Last sequence update)
DT      25-OCT-2004 (Rel. 45, Last annotation update)
DE      Enterotoxin type E precursor (SEB).
GN      Name=entc;
OS      Staphylococcus aureus.
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX      NCBI_TaxID=1280;
RN      [1]
RP      SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
RC      STRAIN=MUR265;
RX      MEDLINE=88257005; PubMed=3384800;
RA      Couch J.L., Solis M.T., Betley M.J.;
RT      "Cloning and nucleotide sequence of the type E staphylococcal
RT      enterotoxin gene.";
RL      J. Bacteriol. 170:2954-2960 (1988).
RN      [2]
RP      3D-STRUCTURE MODELING.
RX      MEDLINE=96022987; PubMed=7552730;
RA      Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
RT      "Residues defining V beta specificity in staphylococcal
RT      enterotoxins.";
RL      Nat. Struct. Biol. 2:680-686 (1995).
CC      -I- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC      staphylococcal food poisoning syndrome. The illness characterized
CC      by high fever, hypotension, diarrhea, shock, and in some cases
CC      death.
CC      -I- CORFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC      for the toxin interaction with MHC class II (by similarity).
CC      -I- SUBCELLULAR LOCATION: Secreted.
CC      -I- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC      family.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@ebi.ac.uk).
CC      -----

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EMBL: M21319; AAA26617.1; -
 DR PIR: A28179; A28179.28-257.
 DR PDB: 1SBE; Model: @28-257.
 DR InterPro: IPR008992; Bact_endotox.
 DR InterPro: IPR006177; Bact1_tox.
 DR InterPro: IPR01050; Pectin_lyas_1like.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006126; Staph/Strep_tox.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF02876; Scap_stp_tox; 1.
 DR Pfam: PF01123; Scap_stp_toxin; 1.
 DR PRINTS: PR00279; BACTR1TOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR 3D-structure; Direct protein sequencing; Enterotoxin; Metal-binding;
 KM Signal; Superaantigen; Toxin; Zinc.
 FT SIGNAL 1 27
 FT CHAIN 28 257 Enterotoxin type E.
 FT METAL 211 211 Zinc (By similarity).
 FT METAL 249 249 Zinc (By similarity).
 FT METAL 251 251 Zinc (By similarity).
 FT HELIX 33 35
 FT HELIX 39 41
 FT STRAND 42 42
 FT STRAND 46 47
 FT STRAND 48 51
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 FT STRAND 59 64
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 FT TURN 249 257
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 Best Local Similarity 100.0%; Pred. No. 6,6e-94;
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

145 EKKVPINLMIDGKQTVPIPIKVTSKKEVTVOELDQAHYHKGKFGVNSDFGSKVQ 204
 DB
 QY 181 RGLIVFHSSEGSTSYVDLFDAGQGYPTLRLIRPNKNTINSNLHIDLYLTT 233
 DB 205 RGLIVFHSSEGSTSYVDLFDAGQGYPTLRLIRPNKNTINSNLHIDLYLTT 257
 RESULT 2
 ID EXTRA STRAND STANDARD; PRT; 257 AA.
 AC P13163;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Enterotoxin type A precursor (SEA).
 GN Name:entA; Ordered locus names: MW1889;
 OS Staphylococcus aureus (strain MW2), and
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=196620, 1280;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=WM2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.,
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA.";
 RL Lancet 359:1819-1827(2002).
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=FR137;
 RX MEDLINE=88086892; PubMed=3335483;
 RA Beley M.J., Mekalanos J.J.,
 RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene.";
 RL J. Bacteriol. 170:34-41(1988).
 RN
 RP SEQUENCE OF 25-257.
 RX MEDLINE=87222293; PubMed=3584106;
 RA Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.,
 RT "Complete amino acid sequence of staphylococcal enterotoxin A.";
 RL J. Biol. Chem. 262:7006-7013(1987).
 RN
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=95354648; PubMed=7628431;
 RA Schad E.M., Zaitseva I., Zaitsev V.N., Dohlsen M., Kalland T.,
 RA Schlievert P.M., Ohlendorf D.H., Svensson L.A.,
 RT "Crystal structure of the superantigen staphylococcal enterotoxin type
 A.";
 RL EMBO J. 14:3292-3301(1995).
 RN
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=97113025; PubMed=8943278; DOI=10.1074/jbc.271.50.32212;
 RA Sundstroem M., Hallen D., Svensson A., Schad E., Dohlsen M.,
 RA Abrahamson L.,
 RT "The Co-crystal structure of staphylococcal enterotoxin type A with
 RT Zn2+ at 2.7-A resolution. Implications for major histocompatibility
 RT complex class II binding.";
 RL J. Biol. Chem. 271:32212-32216(1996).
 RN
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F., Jr., Fletcher J., Sax M.,
 RT "Residues defining V beta specificity in staphylococcal
 RT enterotoxins.";
 RL Nat. Struct. Biol. 2:680-686(1995).
 RN
 RP COMPARISON OF STRUCTURE OF SEA AND SECC.
 RX MEDLINE=97334373; PubMed=9191070; DOI=10.1006/jmbi.1997.1023;
 RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.,
 RT "A structural and functional comparison of staphylococcal enterotoxins

RT A and C2 reveals remarkable similarity and dissimilarity.";
RL J. Mol. Biol. 269:270-280 (1997).
CC -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -1- CORPACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MISCELLANEOUS: This toxin seems to be coded by a bacteriophage.
CC -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AP004828; BAB95754.1; -.
DR EMBL; M18970; AAA26681.1; -.
DR PIR; A28664; A28664. -.
DR PDB; 1D1Q; X-ray; A=24-257.
DR PDB; 1ESF; X-ray; A/B=-.
DR PDB; 1I4G; X-ray; A/B=25-257.
DR PDB; 1I4H; X-ray; A/B=25-257.
DR PDB; 1LO5; X-ray; D=25-257.
DR PDB; 1SEA; Model; @=25-257.
DR PDB; 1SXT; X-ray; A/B=25-257.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; BactI_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Scap_Scrlp_toxin; 1.
DR Pfam; PF01123; Scap_Scrlp_toxin; 1.
DR PRINTS; PR00279; BACTR1TOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW 3D-structure; Complete proteome; Direct protein sequencing;
KW Enterotoxin; Metal-binding; Signal; Superantigen; Toxin; Zinc.
FT CHAIN 1 24 Enterotoxin type A.
FT DISULFID 120 130
FT METAL 211 211 Zinc.
FT METAL 249 249 Zinc.
FT METAL 251 251 Zinc.
FT CONFLICT 242 242 T -> S (in Ref. 3).
FT HELIX 33 35
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FT STRAND 158 160

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SQ SEQUENCE 257 AA; 29669 MW; ADEBFSBCA1F14677 CRC64;
Query Match 82.6%; Score 1023; DB 1; Length 257;
Best Local Similarity 82.0%; Pred. No. 3,4e-76;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEXKDLRKSEIQRNALNLRQIYYNEKATENKESDDQPLENTLLFKGPTG 60
DB 25 SEKSEINEXKDLRKSEIQRNALNLRQIYYNEKATENKESDDQPLENTLLFKGPTD 84
QY 61 HPWYNDLLVDLGSXDATNKYKQKVDLYGAYYQACAGTPTNKTAQMGVYTLHDNNELT 120
DB 85 HSWYNDLLVDLFDSDIDVYKQKQVDLYGAYYQACAGTPTNKTAQMGVYTLHDNNELT 144
QY 121 EEKYPINLWIDGKQTTYPIDRKVTSKKEVTVOELDLQARYHLGKGLYNSDSFGKQVQ 180
DB 145 EEKYPINLWIDGKQTTYPIDRKVTSKKEVTVOELDLQARYHLGKGLYNSDSFGKQVQ 204
QY 181 RGLVYFHSSEGSTSYDLFDAQGYPTLRIYRDNKTINSENLHIDLYTT 233
DB 205 RGLVYFHSSTEPSVNYDLFGAQGISNTLRIYRDNKTINSENLHIDLYTT 257
RESULT 3
ID 06G7Y7 PRELIMINARY; PRT; 257 AA.
AC 06G7Y7
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin type A.
GN OrderedLocustNames=SAS1872;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=282459;
RN [1]
RP SEQUENCE FROM N. A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.V., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurel L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cronin C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagele K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571857; CAG43678.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; BactI_tox.
DR InterPro; IPR006123; Scap/Scrlp_toxin.

DR InterPro: IPR006126; Staph/Strep_tox.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF01123; Staph_Strep_toxin_1.
 DR Pfam: PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR Complete proteome.
 SQ SEQUENCE 257 AA; 29669 MW; ADBEFSECALP14677 CRC64;

Query Match 82.6%; Score 1023; DB 2; Length 257;
 Best Local Similarity 82.0%; Pred. No. 3.4e-76;
 Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTD 84
 QY 61 HSWYNDLVLDGSKATNKYKKKVDLYGAYGYOCAGGTPNKTKACMGVTLHDNNRLT 120
 DB 85 HSWYNDLVLDGSKATNKYKKKVDLYGAYGYOCAGGTPNKTKACMGVTLHDNNRLT 144
 QY 121 EEKVPINIMIDGKQTPVIDKYTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVVQ 180
 DB 145 EEKVPINIMIDGKQTPVIDKYTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVVQ 204
 QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIDLYLTT 233
 DB 205 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIDLYLTT 257

RESULT 4
 Q931M4 PRELIMINARY; PRT; 260 AA.

AC Q931M4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 25, Last annotation update)
 DE Enterotoxin P.
 GN Name=sep; OrderedlocusNames=SAV1948;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=158878;
 RX STRAIN=Mu50 / ATCC 700699;
 MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani U. Y., Takahashi N. K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuuchi J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi K., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus".
 RT Lancet 357:1225-1240(2001).
 RL EMBL: AP003364; BABS8110.1; -.
 DR HSSP: P13163; ILO5.
 DR GO: GO:000576; C:extracellular; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR008992; Bact_endotox.
 DR InterPro: IPR006177; Bactrl_tox.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006126; Staph/Strep_tox.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF01123; Staph_Strep_toxin_1.
 DR Pfam: PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 260 AA; 30016 MW; 15C2D36270F8B241 CRC64;

Query Match 82.6%; Score 1023; DB 2; Length 260;
 Best Local Similarity 81.5%; Pred. No. 3.5e-76;
 Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 DB 28 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTD 87
 QY 61 HSWYNDLVLDGSKATNKYKKKVDLYGAYGYOCAGGTPNKTKACMGVTLHDNNRLT 120
 DB 88 HSWYNDLVLDGSKATNKYKKKVDLYGAYGYOCAGGTPNKTKACMGVTLHDNNRLT 147
 QY 121 EEKVPINIMIDGKQTPVIDKYTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVVQ 180
 DB 148 EEKVPINIMIDGKQTPVIDKYTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVVQ 207
 QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIDLYLTT 233
 DB 208 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIDLYLTT 260

RESULT 5
 Q6GFA8 PRELIMINARY; PRT; 257 AA.

AC Q6GFA8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Enterotoxin type A.
 GN OrderedlocusNames=SA2043;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=282458;
 RX STRAIN=MRSA252;
 MEDLINE=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Feltwell T., Hance Z., Harris B., Hauser A., Holtrov S., Jagels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.,
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance."
 RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 RL EMBL: BX571856; CAG41028.1; -.
 DR GO: GO:000576; C:extracellular; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR008992; Bact_endotox.
 DR InterPro: IPR006177; Bactrl_tox.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006126; Staph/Strep_tox.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF01123; Staph_Strep_toxin_1.
 DR Pfam: PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 257 AA; 29674 MW; 56B0A6D952BDFED4 CRC64;

Query Match 81.8%; Score 1013; DB 2; Length 257;
 Best Local Similarity 81.5%; Pred. No. 3.3e-75;
 Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTD 84

Qy		HPWVNDLLVDLGSKATNKYKKGVLDLYAAYYGCAAGTTPKTKACMGAVTLTHDNNRLT	120
Dy		HSWNIDDLVDFDSKOIVDKRKRKDVLGYAYYGCAAGTTPKTKACMGAVTLTHDNNRLT	144
Qy		EEKVPINIMIDGCKQTVPVIDRKVTSKEEVTVOELDLQARHYLHGFGGLYNSDFSQKVQ	180
Dy		EKKKPINIMIDGCKONTVALEFVKTNKRNVTVQVELDLQARRYLQEKXNLYNSDVDFGKVQ	204
Qy		RGLVFHSSEGSTVSVDLPDAGGVPTDLLRYRDNKTINSENHLHDLVLTXT	233
Dy		RGLVFHTSTEPSVNVDLPFAGAGGNNTLLRIYRDNKTINSENHMIDVLYLTS	257
 RESULT 6 Q99SU3 PRELIMINARY; PRT; 260 AA.			
ID	Q99SU3		
AC	Q99SU3.		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DE	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Enterotoxin P.		
GN	Name=sep; OrderedLocustNames=SA1761;		
OS	Staphylococcus aureus (strain N315).		
OC	Bacteria, Firmicutes, Bacillales, Staphylococcaceae.		
OX	NCBI_taxid=158879;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=N315;		
RX	MEDLINE=2311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;		
RA	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,		
RA	Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,		
RA	Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,		
RA	Mitsutani-Ii Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,		
RA	Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuaki J.,		
RA	Kanehisa M., Yamashita A., Oshima K., Futuya K., Yoshino C., Shiba T.,		
RA	Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;		
RT	"Whole genome sequencing of methicillin-resistant Staphylococcus		
RT	aureus."		
RL	Lancef_357:1225-1240(2001).		
DR	EMBL, AF003135, BAB43036.1, --		
DR	PIR, C89984; C89984.		
DR	HSSP, P13163; ISXT.		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPRO08992; Bact_endocox.		
DR	InterPro; IPRO06177; BcctI_tox.		
DR	InterPro; IPRO06123; Scap/Strep_toxin.		
DR	InterPro; IPRO06126; Staph/Strept_tox.		
DR	InterPro; IPRO06173; Staph_cox_OB.		
DR	Pfam; PF01123; Scap_strep_toxin; 1.		
DR	Pfam; PF02876; Scap_strep_tox_C; 1.		
DR	PRINTS; PR00279; BACTRTOXIN-		
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.		
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.		
KW	Complete proteome.		
QO	SEQUENCE 260 AA; 29708 MW; 087C5B4EC028CFDB CRC64;		

Query Match	80.3%	Score 994	DB 2	Length 260
Best Local Similarity	79.0%	Pred. No. 8.5e-74		
Matches 184	Conservative 17	Matches 32	Indels 0	Gaps 0
QY	1	SEKSEINEKRLRKSSELOJRNALSNLRQIYYNEKAITENKESDDOFLENTLLFGKFTG	60	
Db	28	SEKSEINGKLOLQKSELOJRNALSNLRQIYYNEKAITENKESDDOFLNTLLFPDFTG	87	
QY	61	HPWYNDLLVLDLGSKDATNKKYGGKVDLYGAYYGYOAGGTPNKTAQMGYVTLHDNNRLT	120	
Db	88	HOWYNDLLVLDLGSKDTANIKYGGKVDLYGAYYGYOAGGTPPKTACMGYVTLHDNNQLE	147	
QY	121	EEKKVPINLMDGKQTYPIPIDKVTSSKEVTVQELDLQARHLHKGFLGYNDSFGKQ	180	
Db	148	EEKKVPINLMDGKQNTVPILGVTKNNKKEVTVQELDLQARHLHETVLYNIDNFGKQ	207	

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QY      181 RGLIVHSSEGSIVSYDLFDAGQGYPTLLRIYRDNKTINSENHIDLYLTT 233
      ||||| : ||||| ||||| ||||| : ||||| |||||
DB      208 RGLIEFHPSSEGSVGYDLFGAQQGYPTQLRIYRDNKTIKSKNHIDLYLTT 260
```

RESULT 7

ID	Q6XZB9	PRELIMINARY;	PRT;	219 AA.
AC	Q6XZB9			
DT	05-JUL-2004	(TREMBLrel_27, Created)		
DT	05-JUL-2004	(TREMBLrel_27, Last sequence update)		
DT	05-JUL-2004	(TREMBLrel_27, Last annotation update)		
DE	Enterotoxin sea variant (Fragment).			
OS	Staphylococcus aureus			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus			
NCBI_taxid=1280;				

RP SEQUENCE FROM N.A.
RC STRAIN=330E;
RX MELUNIB=22944091; PubMed=14580397; DOI=10.1016/S0890-8508(03)00058-6
RA "Leterrier C., Petelle S., Dillasser F., Fach P,
RT "A strategy based on 5' nuclease multiplex PCR to detect enterotoxin
RT genes sea to sea of *Staphylococcus aureus*.";
RL Mol. Cell. Probes 17:227-235(2003) .
DR EMBL; AY196686; AAP37183.1; "
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006892; Bact_endotox.
DR InterPro; IPR006177; Bact_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Scrlp_toxin_1
DR Pfam; PF00876; Staph_Scrlp_tox_C_1.
DR PRINTS; PR00279; BACTRLTOXIN
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00276; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 219 AA; 25264 MW; DE8E38ABE652FC89 CRC64;

Query Match	78.4%	Score 971	DB 2	Length 219
Best Local Similarity	82.6%	Pred. No. 5.4e-72		
Matches 180	Conservative 17	Mismatches 21	Indels 0	Gaps 0

Qy	9	EKLRRKSELSQRNALSNLFOIYYNEBKAITENKESDDOLFENTLLTFKGFPLGHMAYNDL	68
Db	2	EKLHKKSELQGVALLNNLKFOIYYNHGKALITENKESDNOFLDHITLFNSSFPTDHPMYNDL	61
Qy	69	VDLGSKDATNRKYGGKKVLDYGAIVYGOCAGGPNNKTACMGSGVTLLHDNNRLTEEEKYPIN	128
Db	62	VDPDSKVLAADTKYGGKKVLDYGAIVYGCAGGIPNNKTACMGSGVTLLHDNNRLTEEEKYPIN	122
Qy	129	LWIDGKQTVPVIDKVTSSKCEVTVQELDIQARHYLHGKFGLYNSDSPCGKTYQRGILYFHS	186
Db	122	LWIDGKQNTVPLETVKTNKECVTVQELDIQARHYLHGKXYLYNSDTPFGKTYQRGILYFHT	181
Qy	189	SBSGSTSYDLFDAQGQGYPDTLRIYRDNKTINSSELIH	226
Db	182	STEPSVNYDLFGAQGQYSNTLLRIYRDNKTINSSEMH	219

RESULT 8

ID Q76LS7 PRELIMINARY; PRT; 268 AA

DT	05-JUN-2004	(TREMblrel. 27, Created)
DT	05-JUN-2004	(TREMblrel. 27, Last sequence update)
DT	05-JUN-2004	(TREMblrel. 27, Last annotation update)
DE	Enterotoxin J.	
GN	Name=ej;	
OC	Staphylococcus aureus	
CC	Bacteria; Firmicutes; Bacillales; Staphylococcus.	

NCBI_TaxID=1280;
RN SEQUENCE FROM N.A.
RP Omoe K., Hu D., Nakane A., Shinagawa K.;
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB075606; BAC97796.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pachogoneis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 268 AA; 31257 MW; 016E5346079D3E20 CRC64;

Query Match 67.6%; Score 837; DB 2; Length 268;
Best Local Similarity 65.4%; Pred. No. 7.6e-61;
Matches 151; Conservative 38; Mismatches 42; Indels 0; Gaps 0;

QY 3 KEEIENKDLRKSEIQRNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFTGHP 62
DB 27 KHEITKEKHLHKKSELSITLNNLRHIFPENEKISEKMTDQFLDYTLLEKSPFISHS 86
QY 63 WYNDLLVDGSKDATTNKYKGVLDYGAAYGYOCAGGTPNKTAQMGVTLHDNNRLTEB 122
DB 87 QYNDLLVQDSKETVWKFKGQVDLYGSYGFQCSGSKPKTKACMGVTLHNNQLYDT 146
QY 123 KKVPIMLWIDGKQTVPIDKVTSSKEVTVQELDQARHYLHGKFGLYNSDSFGKVGQK 182
DB 147 KKVPIMLWIDSIKTVPLDIVTKNNKKVITQELDQARHYLHGQVLYNSPSTFGKIQK 206
QY 183 LIVFHSSEGSTVSYDLFDAQGYPTDLRIYRDNKTINSNHLIDLYTT 233
DB 207 LIVFHTSKPELVSYDLFNVIGYPTDLKIKYODNKIIESENHIDILYLTYS 257

RESULT 9
ID 085217 PRELIMINARY; PRT; 268 AA.
AC 085217;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Enterotoxin J.
GN Name=sej;
OS Staphylococcus aureus.
OG Plasmid p18485.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN SEQUENCE FROM N.A.
RP STRAIN=KS11410;
RX MEDLINE=99052098; PubMed=9835033;
RA Zhang S., Iandolo J.J., Stewart G.C.;
RT "The enterotoxin D plasmid of Staphylococcus aureus encodes a second
enterotoxin determinant (sej).";
RL FEMS Microbiol. Lett. 168:227-233 (1998).
DR HSSP; P13163; IESP.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pachogoneis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.

DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Plasmid.
SQ SEQUENCE 268 AA; 31230 MW; ACSF3546060ACE22 CRC64;

Query Match 67.0%; Score 830; DB 2; Length 268;
Best Local Similarity 64.9%; Pred. No. 2.9e-60;
Matches 150; Conservative 38; Mismatches 43; Indels 0; Gaps 0;

QY 3 KEEIENKDLRKSEIQRNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFTGHP 62
DB 27 KHEITKEKHLHKKSELSITLNNLRHIFPENEKISEKMTDQFLDYTLLEKSPFISHS 86
QY 63 WYNDLLVDGSKDATTNKYKGVLDYGAAYGYOCAGGTPNKTAQMGVTLHDNNRLTEB 122
DB 87 QYNDLLVQDSKETVWKFKGQVDLYGSYGFQCSGSKPKTKACMGVTLHNNQLYDT 146
QY 123 KKVPIMLWIDGKQTVPIDKVTSSKEVTVQELDQARHYLHGKFGLYNSDSFGKVGQK 182
DB 147 KKVPIMLWIDSIKTVPLDIVTKNNKKVITQELDQARHYLHGQVLYNSPSTFGKIQK 206
QY 183 LIVFHSSEGSTVSYDLFDAQGYPTDLRIYRDNKTINSNHLIDLYTT 233
DB 207 LIVFHTSKPELVSYDLFNVIGYPTDLKIKYODNKIIESENHIDILYLTYS 257

RESULT 10
ID 06R2G0 PRELIMINARY; PRT; 154 AA.
AC 06R2G0;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Enterotoxin B (Fragment).
OS Staphylococcus aureus subsp. aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=46170;
RN SEQUENCE FROM N.A.
RP STRAIN=ATCC 27664;
RX PubMed=15131181;
RA Sergeev N., Volokhov D., Chizhikov V., Rasooly A.;
RT "Simultaneous analysis of multiple staphylococcal enterotoxin genes by
an oligonucleotide microarray assay.";
RL J. Clin. Microbiol. 42:2134-2143 (2004).
DR EMBL; AY518387; AAR9635.1; -
DR HSSP; P13380; IANB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pachogoneis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 154
SQ SEQUENCE 154 AA; 17390 MW; 10D3229E23F0C74F CRC64;

Query Match 66.6%; Score 825; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 3.8e-60;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 ATKYKGGKVDLYGAAYGYOCAGGTPNKTAQMGVTLHDNNRLTEBKVPINLWIDGK 135
DB 1 ATKYKGGKVDLYGAAYGYOCAGGTPNKTAQMGVTLHDNNRLTEBKVPINLWIDGK 60
QY 136 TYVPIDKVTSSKEVTVQELDQARHYLHGKFGLYNSDSFGKVGQGLIVFHSSEGSTVS 195


```
Db 61 TTVPIDKRTSKREVTYVELDQARHYLHGKFGLYNSDSFGKVGRLIVFHSSEGSTVS 120
QY 196 YDLFPAGQYPTTLRIYRDNKTINSENHIDLY 229
Db 121 YDLFPAGQYPTTLRIYRDNKTINSENHIDLY 154

RESULT 11
ETXD STAAU STANDARD: PRT: 258 AA.
ID _ETXD STAAU STANDARD: PRT: 258 AA.
AC P20723;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Enterotoxin type D precursor (SED).
GN Name:entd;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89359112; PubMed=2549000;
RA Bayles K.W., Iandolo J.J.;
RT "Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin D.";
RL J. Bacteriol. 171:4799-4806(1989).
RN [2]
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX STRAIN=ATCC 23235; PubMed=9003758;
RA Sundstroem M., Arntzen L., Antonsson P., Mehndate K., Mourad W., Dohlsten M.;
RT "The crystal structure of staphylococcal enterotoxin type D reveals Zn2+-mediated homodimerization.";
RL EMBO J. 15:6832-6840(1996).
CC -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.
CC -1- SUBUNIT: Homodimer; zinc-dependent.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M28521; AAB06195.1; -.
DR PIR; A33953; A33953.
DR HSSP; P13163; ISXT.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_Strep_tox_C1.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PS00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN; 1.
DR Enterotoxin; Signal; Superantigen; Toxin; Zinc.
FT SIGNAL 1 25
FT CHAIN 26 258 Enterotoxin type D.
FT METAL 212 212 Zinc.
FT METAL 250 250 Zinc.
FT METAL 252 252 Zinc.
FT VARIANT 114 114 P -> A (in strain ATCC 23235).
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SQ SEQUENCE 258 AA; 29746 MW; 4F7C6A28D42597FD CRC64;
Query Match 53.6%; Score 663; DB 1; Length 258;
Best Local Similarity 54.5%; Pred. No. 1.6e-46;
Matches 126; Conservative 35; Mismatches 70; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSEIQRNALSNLRQIYYNEKAITENKESDDQFLENTLLPRGFTG 60
Db 26 NENIDSVKEKELHKKSEISTALNNMKISYADKNPITIGENKSTGDQFLENTLLYKRFPTD 85
QY 61 HPWYNDLLVDGSKDATNKKYKKVDLYGAYYGQACGTPNKTACWGGVTLHDNNRLT 120
Db 86 LIPEDLLINNSKEMAHFYSKAVDYPPIYSINCYGSELDRATCTGCTPHBGNLTK 145
QY 121 EEKVPINLWIDKQGTVPIDKVTSSKKEVTYVELDQARHYLHGKFGLYNSDSFGKRVQ 180
Db 146 ERKKIPINLWINGVQKEVSLDKVQTDKKKNTVQGEIDQARRYLQNDLTLNNYDITGKIQ 205
QY 181 RGLIVFHSSEGSTVSYDLFPAGQYPTTLRIYRDNKTINSENHIDLY 231
Db 206 RGLIEFSSDSKVSYDLFPVKGDFPEKQRLIYSDNKTLSLTHLHIDLY 256

RESULT 12
QGR2F9 PRELIMINARY; PRT: 152 AA.
ID QGR2F9;
AC QGR2F9;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin D (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 10656;
RA Sergeev N., Volokhov D., Chizhikov V., Rasooly A.;
RT "Simultaneous analysis of multiple staphylococcal enterotoxin genes by an oligonucleotide microarray assay.";
RL J. Clin. Microbiol. 42:2134-2143(2004).
DR EMBL; AY518388; AAB99636.1; -.
DR HSSP; P13380; IAN8.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C1.
DR PRINTS; PS00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN; 1.
FT NON_TER 1 152
FT NON_TER 152 152
SQ SEQUENCE 152 AA; 17514 MW; F0354318924CB739 CRC64;
Query Match 40.1%; Score 496; DB 2; Length 152;
Best Local Similarity 59.9%; Pred. No. 4.8e-33;
Matches 91; Conservative 22; Mismatches 39; Indels 0; Gaps 0;
QY 80 YKGGKVDLYGAYYGQACGTPNKTACWGGVTLHDNNRLTEKKVPINLWIDKQGTVP 139
Db 1 FKSKNVDYAIRYSINCTGSEIDRTACTYGGVTPHBGKLEKRRKIPINLWINGVQKEVS 60
QY 140 IDKVTSSKKEVTYVELDQARHYLHGKFGLYNSDSFGKVGRLIVFHSSEGSTVSYDLF 199
Db 61 LDKVQTDKKKNTVQGEIDQARRYLQNDLTLNNYDITGSKIQRGKIEFSSDSKVSYDLF 120
QY 200 DAGQYPTTLRIYRDNKTINSENHIDLY 231
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Db 121 DVGDFPEKQRLRYSDNKTSLSTREHLHIDLYLX 152

RESULT 13

Q8NM97 PRELIMINARY; PRT; 229 AA.

AC 08NM97; PRELIMINARY; PRT; 229 AA.
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE MM1552 protein.
 GN OrderedlocusNames=MM1552;
 OS Staphylococcus aureus (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=156620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2;
 RX MEDLINE=22040717; PubMed=12043378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RA "Genome and virulence determinants of high virulence community-
 RT acquired MRSA";
 RL Lancet 359:1819-1827(2002).
 DR EMBL; AP004827; BAB95417.1; -.
 DR HSP; P13163; ISXT.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bactl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph/Strep_tox.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR KW Complete proteome.
 SQ SEQUENCE 229 AA; 26728 MW; AD3DAF9EALAE3677 CRC64;

Query Match 39.6%; Score 490.5; DB 2; Length 229;
 Best Local Similarity 39.4%; Pred. No. 2.2e-32;
 Matches 91; Conservative 48; Mismatches 87; Indels 5; Gaps 3;

QY 1 SEKSEINERKDKRKSELDONALSNLRQIYYNEKAITENKESDDPLENTLLFKGFFTG 60
 Db 2 TNSASAIERYSDLHNSKFPDSKRLSNK-MSFINPTOL-ENKATNDRLKHDLDFHDMFTN 59
 QY 61 HPWYNDLVDLGSKDATNKYKGVLDYGAUYGYOCAGTTPNKTCACMYGGVTLHNNRLT 120
 Db 60 DMKKDFKVEFENALSKFINKIDIDIFAGNYGCGGATGATNTQCSYGVTLSDNNKYD 119
 QY 121 EEKVPINIMDGKQTPVIDKYTSKKEVTVQELDLQARHYLHGKFGLYNSPFGKVQ 180
 Db 120 DYKNIPCNMIDGQAEIELTAVTKTKKIVTIQELDVQLRNYINERKYLEQ---GGDIV 176
 QY 181 RGLIVHSSGSGTVSYDLDPDAGQYPTLLRIYRDKNTINSENLHIDLYLX 231
 Db 177 KGVYKYNHNDDEONIEYFNINLNGEYEVALKMYADNKTINSKDLHIDLYL 227

RESULT 14

Q6G8W7 PRELIMINARY; PRT; 229 AA.

AC 06G8W7; PRELIMINARY; PRT; 229 AA.
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Putative enterotoxin.
 GN OrderedlocusNames=SA51538;

OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=282459;
 RN [1]

RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell B.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Bason N.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Churche C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA James K.D., Leonard N., Line A., Mayes R., Moulie S., Mungall K.,
 RA Ormond D., Quinn M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance."
 RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 DR EMBL; BX571857; CAG43339.1; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bactl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph/Strep_tox.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR KW Complete proteome.
 SQ SEQUENCE 229 AA; 26728 MW; AD3DAF9EALAE3677 CRC64;

Query Match 39.6%; Score 490.5; DB 2; Length 229;
 Best Local Similarity 39.4%; Pred. No. 2.2e-32;
 Matches 91; Conservative 48; Mismatches 87; Indels 5; Gaps 3;

QY 1 SEKSEINERKDKRKSELDONALSNLRQIYYNEKAITENKESDDPLENTLLFKGFFTG 60
 Db 2 TNSASAIERYSDLHNSKFPDSKRLSNK-MSFINPTOL-ENKATNDRLKHDLDFHDMFTN 59
 QY 61 HPWYNDLVDLGSKDATNKYKGVLDYGAUYGYOCAGTTPNKTCACMYGGVTLHNNRLT 120
 Db 60 DMKKDFKVEFENALSKFINKIDIDIFAGNYGCGGATGATNTQCSYGVTLSDNNKYD 119
 QY 121 EEKVPINIMDGKQTPVIDKYTSKKEVTVQELDLQARHYLHGKFGLYNSPFGKVQ 180
 Db 120 DYKNIPCNMIDGQAEIELTAVTKTKKIVTIQELDVQLRNYINERKYLEQ---GGDIV 176
 QY 181 RGLIVHSSGSGTVSYDLDPDAGQYPTLLRIYRDKNTINSENLHIDLYLX 231
 Db 177 KGVYKYNHNDDEONIEYFNINLNGEYEVALKMYADNKTINSKDLHIDLYL 227

RESULT 15

Q7A2Q6 PRELIMINARY; PRT; 258 AA.

AC Q7A2Q6; PRELIMINARY; PRT; 258 AA.
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Enterotoxin.
 GN Name=sen; OrderedlocusNames=SAV1825;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

RA Mutant-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaio C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL, AP003363; BAB57987.1; -
DR GO, GO:0005576; C:extracellular; IEA.
DR GO, GO:0009405; P:pathogenesis; IEA.
DR InterPro, IPR006177; Bactr1_tox.
DR InterPro, IPR006123; Staph/Strep_toxin.
DR InterPro, IPR006126; Staph/Strep_tox.
DR InterPro, IPR006173; Staph_tox_OB.
DR Pfam, PF01123; Staph_stp_toxin_1.
DR Pfam, PF02876; Staph_stp_tox_C_1.
DR PRINTS, PR00279; BACTRLTOXIN.
DR PROSITE, PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE, PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 29676 MW; 8A6C074F3E1F82D2 CRC64;

Query Match 37.3%; Score 461.5; DB 2; Length 258;
Best Local Similarity 41.2%; Pred. No. 6.4e-30;
Matches 96; Conservative 45; Mismatches 77; Indels 15; Gaps 6;
QY 6 EINEKDLAKKSELQGNALSNLRQIYYNEKAIT-----ENKESDQPLENTLLPFKGFPTG 60
DB 32 EVDKDKLKKKSDLDSSKLFNLTLS--YYTD--ITWQDLSNKISTDQLNNTIILKNIDIS 87
QY 61 HPWYNDDLVDLGSXDATNKKYKGVLDYGAAYGYQACAGTPNKTAQMGVTLHDNNRLT 120
DB 88 VLKTSLSLKVEFNSSDLANQFGKNIDYGLYFGNKCGLTEKTSCLYGVTHDGNQLD 147
QY 121 EEKVPINLMDGKQTTPIDKVTSKKEVTYQELDQARHYLHGKFLYNSDSFGKQV 180
DB 148 EEKYGAVNVPFGDVGQEGFV--IKTKKAKVTYQELDTVRFLNLYKIKYNDT--GNIQ 203
QY 181 RGLIVFHS--SEGTSVSYDLFDAGQVPTLLRLIYRDNKNTINSENLHIDLVL 231
DB 204 KGCIFFSHNNQDQSFYIDLNVKGSVGAEPFQYSDNRKTVSSSNVHIDVFLY 256

RESULT 16
Q7A4X1 PRELIMINARY; PRT; 258 AA.
AC Q7A4X1;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin Sen.
GN Name=sen; OrderedLocustNames=SA1643;
OS *Staphylococcus aureus* (strain N315).
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama T., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito Y.,
RA Kanamori M., Matsumaru H., Matuyama A., Murakami H., Hosoyama A.,
RA Mutant-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaio C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL, AP003363; BAB42911.1; -
DR GO, GO:0005576; C:extracellular; IEA.
DR GO, GO:0009405; P:pathogenesis; IEA.
DR InterPro, IPR006177; Bactr1_tox.

DR InterPro, IPR006177; Bactr1_tox.
DR InterPro, IPR006123; Staph/Strep_toxin.
DR InterPro, IPR006126; Staph/Strep_tox.
DR InterPro, IPR006173; Staph_tox_OB.
DR Pfam, PF01123; Staph_stp_toxin_1.
DR Pfam, PF02876; Staph_stp_tox_C_1.
DR PRINTS, PR00279; BACTRLTOXIN.
DR PROSITE, PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE, PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 29676 MW; 8A6C074F3E1F82D2 CRC64;

Query Match 37.3%; Score 461.5; DB 2; Length 258;
Best Local Similarity 41.2%; Pred. No. 6.4e-30;
Matches 96; Conservative 45; Mismatches 77; Indels 15; Gaps 6;
QY 6 EINEKDLAKKSELQGNALSNLRQIYYNEKAIT-----ENKESDQPLENTLLPFKGFPTG 60
DB 32 EVDKDKLKKKSDLDSSKLFNLTLS--YYTD--ITWQDLSNKISTDQLNNTIILKNIDIS 87
QY 61 HPWYNDDLVDLGSXDATNKKYKGVLDYGAAYGYQACAGTPNKTAQMGVTLHDNNRLT 120
DB 88 VLKTSLSLKVEFNSSDLANQFGKNIDYGLYFGNKCGLTEKTSCLYGVTHDGNQLD 147
QY 121 EEKVPINLMDGKQTTPIDKVTSKKEVTYQELDQARHYLHGKFLYNSDSFGKQV 180
DB 148 EEKYGAVNVPFGDVGQEGFV--IKTKKAKVTYQELDTVRFLNLYKIKYNDT--GNIQ 203
QY 181 RGLIVFHS--SEGTSVSYDLFDAGQVPTLLRLIYRDNKNTINSENLHIDLVL 231
DB 204 KGCIFFSHNNQDQSFYIDLNVKGSVGAEPFQYSDNRKTVSSSNVHIDVFLY 256

RESULT 17
Q9EZM4 PRELIMINARY; PRT; 258 AA.
AC Q9EZM4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE SEN.
GN Name=sen;
OS *Staphylococcus aureus*.
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A900322;
RX MEDLINE=20571956; PubMed=11123352;
RA Jarrard S., Peyrat M.A., Lim A., Tristan A., Bes M., Mougel C.,
RA Etienne J., Vandenesch F., Bonneville M., Lina G.,
RT "egc, a highly prevalent operon of enterotoxin gene, forms a putative
RT nursery of superantigens in *Staphylococcus aureus*."
RL J. Immunol. 166:669-677(2001).
DR EMBL, AF285760; AAG36956.1; -
DR PIR, H89968; H89968.
DR HSSP, Q53585; 1P77.
DR GO, GO:0005576; C:extracellular; IEA.
DR GO, GO:0009405; P:pathogenesis; IEA.
DR InterPro, IPR006177; Bactr1_tox.
DR InterPro, IPR006123; Staph/Strep_toxin.
DR InterPro, IPR006126; Staph/Strep_tox.
DR InterPro, IPR006173; Staph_tox_OB.
DR Pfam, PF01123; Staph_stp_toxin_1.
DR Pfam, PF02876; Staph_stp_tox_C_1.
DR PRINTS, PR00279; BACTRLTOXIN.
DR PROSITE, PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE, PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 29676 MW; 8A6C074F3E1F82D2 CRC64;

Query Match 37.3%; Score 461.5; DB 2; Length 258;
Best Local Similarity 41.2%; Pred. No. 6.4e-30;

Matches 96; Conservative 45; Mismatches 77; Indels 15; Gaps 6;

QY 6 EINEKDLRKSELOALNSLRQIYYNEKAIT-----ENKESDDQPLENTLLFKGFFTG 60
 Db 32 EVDKDLKKKSDLSKSLFNLTSS--YTTD--ITWQDSESNKISTDQLNNTIILKIDIS 87
 QY 61 HPWYNDLVDLGSKDATNKYKGGKVDLYGAYYGOCAGTTPNKTKACMYGGVTLHDNNRLT 120
 Db 88 VLKTSLSKVEFNSSDLANQFKGNIDYGLYGNKCVGLTEKTSCLYGGVTLHDNQDLD 147
 QY 121 EEKVPINLMIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKGLYNSDFGSKVQ 180
 Db 148 EEKVGIVNVFKDGVQOEGFV--IKTKAKAVTVQELDTKVRFKLEMLYKIKYNNKT--GNIQ 203
 QY 181 RGLIVFHS--SEGSTVSYDLFDAQGYPTTLARIYNDKNTINSENHIDLVL 231
 Db 204 KGCIFPHSHNHQDSFYDLYNVKGSVGAEPFQFYSNDRVTSSNHYHIDVFLY 256

RESULT 18

Q6YCN3 PRELIMINARY; PRT; 251 AA.
 ID 06YCN3;
 AC 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Enterotoxin SEN variant.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=1280;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=3825;
 RA MEDLINE=22692404; PubMed=12807452;
 RA Leteire C., Perelle S., Dilaeser F., Pach P.,
 RT "Identification of a new putative enterotoxin SEU encoded by the egc
 RT cluster of Staphylococcus aureus";
 RL J. Appl. Microbiol. 95:38-43(2003).
 DR EMBL: AY158703; ANO17733.1;
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bactrl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_strep_toxin; 1.
 DR Pfam; PF02876; Staph_strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 SQ SEQUENCE 251 AA; 28806 MW; 1E2966FBFB6BA40 CRC64;

Query Match 36.1%; Score 446.5; DB 2; Length 251;
 Best Local Similarity 39.5%; Pred. No. 1.1e-28;
 Matches 92; Conservative 49; Mismatches 77; Indels 15; Gaps 6;

QY 6 EINEKDLRKSELOALNSLRQIYYNEKAIT-----ENKESDDQPLENTLLFKGFFTG 60
 Db 25 DVDKDLKKKSDLSKSLFNLTSS--YTTD--ITWQDSESNKISTDQLNNTIILKIDIS 80
 QY 61 HPWYNDLVDLGSKDATNKYKGGKVDLYGAYYGOCAGTTPNKTKACMYGGVTLHDNNRLT 120
 Db 81 VLKTSLSKVEFNSSDLANQFKGNIDYGLYGNKCVGLTEKTSCLYGGVTLHDNQDLD 140
 QY 121 EEKVPINLMIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKGLYNSDFGSKVQ 180
 Db 141 EEKVGIVNVFKDGVQOEGFV--IKTKAKAVTVQELDTKVRFKLEMLYKIKYNNKT--GNIQ 196
 QY 181 RGLIVFHS--SEGSTVSYDLFDAQGYPTTLARIYNDKNTINSENHIDLVL 231
 Db 197 KGCIFPHSHNHQDSFYDLYNVKGSVGAEPFQFYSNDRVTSSNHYHIDVFLY 249

RESULT 19

Q6GFN1 PRELIMINARY; PRT; 251 AA.
 ID 06GFN1;
 AC 06GFN1;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DE Enterotoxin.
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=282458;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell B.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
 RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moulie S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 DR EMBL; BX571856; CAG40903.1;
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bactrl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_strep_toxin; 1.
 DR Pfam; PF02876; Staph_strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 251 AA; 28806 MW; 1E2966FBFB6BA40 CRC64;

Query Match 36.1%; Score 446.5; DB 2; Length 251;
 Best Local Similarity 39.5%; Pred. No. 1.1e-28;
 Matches 92; Conservative 49; Mismatches 77; Indels 15; Gaps 6;

QY 6 EINEKDLRKSELOALNSLRQIYYNEKAIT-----ENKESDDQPLENTLLFKGFFTG 60
 Db 25 DVDKDLKKKSDLSKSLFNLTSS--YTTD--ITWQDSESNKISTDQLNNTIILKIDIS 80
 QY 61 HPWYNDLVDLGSKDATNKYKGGKVDLYGAYYGOCAGTTPNKTKACMYGGVTLHDNNRLT 120
 Db 81 VLKTSLSKVEFNSSDLANQFKGNIDYGLYGNKCVGLTEKTSCLYGGVTLHDNQDLD 140
 QY 121 EEKVPINLMIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKGLYNSDFGSKVQ 180
 Db 141 EEKVGIVNVFKDGVQOEGFV--IKTKAKAVTVQELDTKVRFKLEMLYKIKYNNKT--GNIQ 196
 QY 181 RGLIVFHS--SEGSTVSYDLFDAQGYPTTLARIYNDKNTINSENHIDLVL 231
 Db 197 KGCIFPHSHNHQDSFYDLYNVKGSVGAEPFQFYSNDRVTSSNHYHIDVFLY 249

RESULT 20

Q6GFN1 PRELIMINARY; PRT; 254 AA.
 ID 06GFN1;
 AC 06GFN1;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Enterotoxin.

Ordered locus names=SA19121;
 OS *Staphylococcus aureus* (strain MRS252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NX NCBI_TaxID=282458;
 RP SEQUENCE FROM N.A.
 RA PubMed:1521324; DOI=10.1073/pnas.0402521101;
 RX Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Knight M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
 RA Bacon N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
 RA Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Muggall K.,
 RA Omond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Genomes of two clinical *Staphylococcus aureus* strains:
 RT evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 DR EMBL; BX571856; CAG40907.1; -;
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bact_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strep_toxin_1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 254 AA; 29447 MW; E2ECD141E300CD9 CRC64;

Query Match 33.4%; Score 414; DB 2; Length 254;
 Best Local Similarity 40.9%; Pred. No. 5.1e-26;
 Matches 99; Conservative 39; Mismatches 84; Indels 20; Gaps 7;

QY 1 SEKSEIIEKDLRKSEIQRNALSNLRQIYYNEKATENKE-SDQFLENTLFFKGF 59
 DB 23 NEENPKI-EDLCKSSVDIALHNDIDYMRNTINESYTLTEKELDLDLFRNF-- 78
 QY 60 GHPW-----YNDLVLVDSKDATNKYKGGKVDLYGAYYGQAGGTPNKTCMYGVT 112
 DB 79 --TWLDGSAEPKDLKVEFSSSEISKEYFKVDLYGYKAKHGCHQVDTACTYGGVT 136
 QY 113 LHDNNRLTEKKVPIINLMIDGKQTVPIIDKVTISKETVTVQELDQARHYLHGKFGLYNS 172
 DB 137 PHENNKLSPEKPIGVAIVKDNVNVNFTI--VTDDKKVTAQELDIKVRKLNNAVYKLY-- 192
 QY 173 DSFGKVGRLIVFHSSEGSTVS--YDLFDAQGYPTLLRIYRDNKTINSENLIHIDLYL 230
 DB 193 DRMTSDVQKGYIKFHSSEHKSFFYYDLFYIKGNLPDQYLQIYNDNKTIDSVDHIDVYL 252
 QY 231 YT 232
 DB 253 FT 254

RESULT 21
 ID 099746 PRELIMINARY; PRT; 260 AA.
 AC 099746;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Enterotoxin.
 GN Name=seo; OrderedLocusNames=SAV1830; ATCC 700699).
 OS *Staphylococcus aureus* (strain M130 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NX NCBI_TaxID=158878;
 RP SEQUENCE FROM N.A.
 RA PubMed:158878;
 RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki U.,
 RA Katohira M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.;
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
 RT aureus".
 RL Lancet 357:1225-1240(2001).
 DR EMBL; AP003363; BAB57992.1; -;
 DR PIR; B89969; B89969.
 DR HSSP; Q54971; 1BXT.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bact_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strep_toxin_1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 260 AA; 29836 MW; AC927DDCC3E3B8EF CRC64;

RP SEQUENCE FROM N.A.
 RC STRAIN=M130 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki U.,
 RA Katohira M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.;
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
 RT aureus".
 RL Lancet 357:1225-1240(2001).
 DR EMBL; AP003363; BAB57992.1; -;
 DR PIR; B89969; B89969.
 DR HSSP; Q54971; 1BXT.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bact_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strep_toxin_1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 260 AA; 29836 MW; AC927DDCC3E3B8EF CRC64;

Query Match 31.3%; Score 387.5; DB 2; Length 260;
 Best Local Similarity 39.9%; Pred. No. 8e-24;
 Matches 97; Conservative 31; Mismatches 86; Indels 29; Gaps 8;

QY 8 NEKD-----LKKSEIQRNALSNLRQIYYNE----FATENKSSDQFLENTLFFKGF 58
 DB 29 NEEDPKIESLCKSSVPIALHNDIDYMRNTINESYTLTEKELDLDLFRNF-- 84
 QY 59 TGHFW-----YNDLVLVDSKDATNKYKGGKVDLYGAYYGQAGGTPNKTCMYGVT 111
 DB 85 ---NWLDGSAEPKDLKVEFSSSAISKEFLKQTVDIYGYKAKHGCHQVDTACTYGGVT 141
 QY 112 TLHDNNRLTEKKVPIINLMIDGKQTVPIIDKVTISKETVTVQELDQARHYLHGKFGLYNS 171
 DB 142 TPHENNKLSPEKPIGVAIVKDNVNVNFTI--VTDDKKVTAQELDIKVRKLNNAVYKLY-- 198
 QY 172 SDSFGKVGRLIVFHSSEGSTVS--YDLFDAQGYPTLLRIYRDNKTINSENLIHIDLY 229
 DB 199 -DRMTSDVQKGYIKFHSSEHKSFFYYDLFYIKGNLPDQYLQIYNDNKTIDSVDHIDVY 257
 QY 230 LYT 232
 DB 258 LFT 260

RESULT 22
 ID 07A4W6 PRELIMINARY; PRT; 260 AA.
 AC 07A4W6;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Enterotoxin Seo.
 GN Name=seo; OrderedLocusNames=SA11648;
 OS *Staphylococcus aureus* (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NX NCBI_TaxID=158879;
 RP SEQUENCE FROM N.A.
 RA PubMed:158879;
 RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki U.,
 RA Katohira M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.;
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
 RT aureus".
 RL Lancet 357:1225-1240(2001).
 DR EMBL; AP003363; BAB57992.1; -;
 DR PIR; B89969; B89969.
 DR HSSP; Q54971; 1BXT.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bact_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strep_toxin_1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 260 AA; 29836 MW; AC927DDCC3E3B8EF CRC64;

Query Match	31.3%	Score 387.5;	DB 2;	Length 260;
Best Local Similarity	39.9%;	Pred. No. 8e-24;		
Matches 97;	Conservative 31;	Mismatches 86;	Indels 29;	Gaps 8;

RESULT 23	
Q9EZM8	PRELIMINARY;
Q9EZM8	PRT; 261 AA

GO; GO:0005576; C:extracellular; IEA

Query Match	31.3%;	Score 387.5;	DB 2;	Length 261;
Best Local Similarity	39.9%;	Pred. No. 8.1e-24;		
Matches 97;	Conservative 31;	Mismatches 86;	Indels 29;	Gaps 8;

RESULT 24	
Q52075	
Q52075	PRELIMINARY;
Q52075	PRT; 179 AA

Query Match	30.8%;	Score 381;	DB 2;	Length 179;
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Best Local Similarity 48.7%, Pred. No. 1.8e-23;
Matches 73; Conservative 24; Mismatches 53; Indels 0; Gaps 0;

QY 1 SEKSEIENEKDLRKSELSORNALNLTROIYYNEKATITENKESDQPLENTLLFKGFTG 60
Db 26 NENIDSVKEKELHKKSELSTRLNMMKSYADKNIIIGENKSTGQPLENTLLFKGFTD 85
QY 61 HPWYNDLLVDLSKDATNRKYGKVDLYGAYYGACGTPNKTCMYGGVTLHDNNRLT 120
Db 86 LINFEDLLINFNSKEMAGFKSKNDVYPIRYSINCYGIEDTACTYGGVTPHEGNKTK 145
QY 121 EEKVPIPLMIDGKQTYPIDKVTSKEV 150
Db 146 ERKKIPINLWINGQKEVSLDKVOTDKNL 175

RESULT 25
Q8RR76 PRELIMINARY; PRT; 217 AA.
AC Q8RR76;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Enterotoxin H (Fragment).
GN Name=seh;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21871379; PubMed=11880405;
RA Omeo K., Ishikawa M., Shimoda Y., Hu D.L., Ueda S., Shinagawa K.;
RT "Detection of seh, seh, and sel genes in Staphylococcus aureus
RT isolates and determination of the enterotoxin productivities of S.
RT aureus isolates Harboring seh, seh, or sel genes.";
RL J. Clin. Microbiol. 40:857-862(2002).
DR EMBL; AB060536; BAB85990.1; -.
DR HSSP; Q53585; IEWC.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactr_tox.
DR InterPro; IPR006173; Staph_toxin.
DR Pfam; PF01123; Staph_stp_toxin.1.
DR Pfam; PF02876; Staph_stp_toxin_C.1.
DR PRINTS; PR00279; BACTRLTOXIN_
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 217 AA; 25143 MW; ABA44E23F31DE80D CRC64;

Query Match 29.6%; Score 366; DB 2; Length 217;
Best Local Similarity 37.9%; Pred. No. 3.8e-22;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;

QY 10 KDLRKSELSORNALNLTROIYYNEKATITENKESDQPLENTLLFKGFTGHPWYNDLLV 69
Db 1 EDLHDKSELDTLALAN--AYGQYNHPIKENTKSDIEGKOLIPRN--QGDSG--NDLRV 55
QY 70 DLGSKDATNRKYGKVDLYGAYYGACGTPNKTCMYGGVTLHDNNRLTBKKVPINL 129
Db 56 KFAADLAQKFKKNKVDIYGASFFYKCEKISENISECYGGTLL--NSEKLAQERYIGANV 114
QY 130 WIDGQTVPIDKVTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGVORGLIVPFS 189
Db 115 WVDGIQKTEL--IRTKGNVTLOGLDIKIRKILSDKIKIYKDS---EISKGLIEFDMK 169
QY 190 EGSFVSYDLFDAGGQYPTLLRIYHNDKNTINSENL--HIDLVLTYT 232
Db 170 TPRDYSFDIYDLKGENDYEIDKIYEDNKTLSDDISHIDVNLTYT 213

RESULT 26

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ETXH STAHM
ID ETXH STAHM STANDARD; PRT; 241 AA.
AC Q53585;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Enterotoxin type H precursor (SEH).
GN Name=entH; Synonyms=seh; Ordered locusNames=MM0051;
OS Staphylococcus aureus (strain MW2), and
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620, 1280;
RN [1]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
RP STRAIN=D4508;
RX MEDLINE=95053699; PubMed=7964453;
RA Ren K., Bannan J.D., Pancholi V., Cheung A.L., Robbins J.C.,
RA Fieschetti V.A., Zabriekie J.B.;
RT "Characterization and biological properties of a new staphylococcal
RT exotoxin.";
RL J. Exp. Med. 180:1675-1683(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Bada T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.69 ANGSTROMS).
RX PubMed=10986116; DOI=10.1006/jmbi.2000.4093;
RA Hakansson M., Petersson K., Nilsson H., Forsberg G., Bjorker P.,
RA Antonsson P., Svensson L.A.;
RT "The crystal structure of staphylococcal enterotoxin H: implications
RT for binding properties to MHC class II and TCR molecules.";
RL J. Mol. Biol. 302:527-537(2000).
CC -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -1- COPACOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U11702; AAA19777.1; -.
DR EMBL; AP004822; BAB93916.1; -.
DR PDB; 1ENP; X-ray; A=26-237.
DR PDB; 1EWC; X-ray; A=26-239.
DR PDB; 1F77; X-ray; A/B=25-241.
DR PDB; 1HXV; X-ray; D=25-237.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactr_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_toxin.
DR Pfam; PF02876; Staph_stp_toxin_C.1.
DR Pfam; PF01123; Staph_stp_toxin.1.
DR PRINTS; PR00279; BACTRLTOXIN_
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

```

3D-structure: Complete proteome; Direct protein sequencing;
KM Enterotoxin; Metal-binding; Signal; Superantigen; Toxin; Zinc.
FT SIGNAL 1 24 Enterotoxin type H.
FT CHAIN 25 241
FT METAL 230 230 Zinc.
FT METAL 232 232 Zinc.
FT DISULFID 106 116
SQ SEQUENCE 241 AA; 27858 MW; 70F77985877616CE CRC64;
Query Match 29.6%; Score 366; DB 1; Length 241;
Best Local Similarity 37.9%; Pred. No. 4.3e-22;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;
QY 10 KDLRKSELDQRLNLSNRQIYYNNEKAITENKESDDQFLFNTLLFPKGFTHPWYNDLLV 69
DB 25 EDLHDKSELTDLALAN--AYGQYNHPFIKENIKSDISEGKDLIFRN--QGDSG-NDLRV 79
QY 70 DLGSKDATNKYKGVKVDLYGAYVYQACAGTPNKTCAMYGVTLLHDNNRLTEKKVPINL 129
DB 80 KRATADLAQKFNKVDIYGASFYKCEKISENISCLYGTTL--NSEKLAQERIVGANV 138
QY 130 WIDGQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVGQRLIVFHS 189
DB 139 WVDGIQKETEL--IRTNKKNVTLOELDIKIRKILSDKRIYKYDSS--EISKGLIEFDK 193
QY 190 EGSSTVSYDLFDAQGYPTLRLIYRDNKTINSENL-HIDLXYLT 232
DB 194 TRDYSFDIYDLKGENDYEDIKIYEDNKTLSKSDISHIDVNLVT 237
RESULT 27
Q6VAM8 PRELIMINARY; PRT; 241 AA.
ID Q6VAM8; 06VAM8;
AC 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Enterotoxin H precursor.
GN Name=seh;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=FRI 137;
RA Gul'ko L.B., Voyushin K.E., Fluer F.S., Okorokova N.A., Krivenko M.S.,
RA Veiko V.P., Debabov V.G.;
RT "The Obtaining of the Tumor-Addressed Genetically Engineered Drug for
RT Cancer Immunotherapy. II. Cloning a Gene of the pro-Enterotoxin H (seh)
RT from Staphylococcus aureus, Its Expression in *Escherichia coli*.
RT Investigation of the Enterotoxin H Secretion by *E. coli* Cells.";
RL Biotechnology 6:172-78(2003).
DR EMBL: AY345144; AA063188.1; -;
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:patogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bactl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_strep_toxin; 1.
DR Pfam: PF02876; Staph_strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR SIGNAL.
KM SIGNAL.
FT CHAIN 25 241 enterotoxin H.
SQ SEQUENCE 241 AA; 27831 MW; 70EBB8418C9BCCE CRC64;
Query Match 29.6%; Score 366; DB 2; Length 241;
Best Local Similarity 37.9%; Pred. No. 4.3e-22;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;
QY 10 KDLRKSELDQRLNLSNRQIYYNNEKAITENKESDDQFLFNTLLFPKGFTHPWYNDLLV 69

DB 25 EDLHDKSELTDLALAN--AYGQYNHPFIKENIKSDISEGKDLIFRN--QGDSG-NDLRV 79
QY 70 DLGSKDATNKYKGVKVDLYGAYVYQACAGTPNKTCAMYGVTLLHDNNRLTEKKVPINL 129
DB 80 KRATADLAQKFNKVDIYGASFYKCEKISENISCLYGTTL--NSEKLAQERIVGANV 138
QY 130 WIDGQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVGQRLIVFHS 189
DB 139 WVDGIQKETEL--IRTNKKNVTLOELDIKIRKILSDKRIYKYDSS--EISKGLIEFDK 193
QY 190 EGSSTVSYDLFDAQGYPTLRLIYRDNKTINSENL-HIDLXYLT 232
DB 194 TRDYSFDIYDLKGENDYEDIKIYEDNKTLSKSDISHIDVNLVT 237
RESULT 28
Q6GD45 PRELIMINARY; PRT; 241 AA.
ID Q6GD45; 06GD45;
AC 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Enterotoxin H.
GN Name=seh; Ordered locus Names=SA50051;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=282459;
RN RN
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T., Dowd L.,
RA Churcher C., Clark L., Cotton A., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical *Staphylococcus aureus* strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
RL EMBL: BX571857; CAG41819.1; -;
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:patogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bactl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_strep_toxin; 1.
DR Pfam: PF02876; Staph_strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KM COMPLETE PROTEOME.
SQ SEQUENCE 241 AA; 27858 MW; 70F77985877616CE CRC64;
Query Match 29.6%; Score 366; DB 2; Length 241;
Best Local Similarity 37.9%; Pred. No. 4.3e-22;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;
QY 10 KDLRKSELDQRLNLSNRQIYYNNEKAITENKESDDQFLFNTLLFPKGFTHPWYNDLLV 69
DB 25 EDLHDKSELTDLALAN--AYGQYNHPFIKENIKSDISEGKDLIFRN--QGDSG-NDLRV 79
QY 70 DLGSKDATNKYKGVKVDLYGAYVYQACAGTPNKTCAMYGVTLLHDNNRLTEKKVPINL 129
DB 80 KRATADLAQKFNKVDIYGASFYKCEKISENISCLYGTTL--NSEKLAQERIVGANV 138
QY 130 WIDGQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVGQRLIVFHS 189
DB 139 WVDGIQKETEL--IRTNKKNVTLOELDIKIRKILSDKRIYKYDSS--EISKGLIEFDK 193


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Qy 190 EGSVSYDLFPAQGYPTTLRLRYDNKTINSENT-HIDLXYT 232
Db 194 TPRDYSFDIYDLKGENDYEIDKIYEDNKTLSDDISHIDVMLYT 237

RESULT 29
Q6YCN5 PRELIMINARY; PRT; 242 AA.
ID Q6YCN5;
AC Q6YCN5;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Enterotoxin SEI variant.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
RX NCI [1]
RP SEQUENCE FROM N.A.
RC STRAIN=382F;
RA MEDLINE=22692404; PubMed=12807452;
RA Leterre C., Perelle S., Dilaeser F., Fach P.,
RT "Identification of a new putative enterotoxin SEU encoded by the egc
RT cluster of Staphylococcus aureus.";
RL J. Appl. Microbiol. 95:38-43(2003).
DR EMBL; AY158703; AA017731.1; -.
DR HSSP; P13380; 1AN8.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bact_T_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_tox_OB.
DR Pfam; PF02876; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRI_TOXIN_
DR PROSITE; PS00278; STRAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 242 AA; 27950 MW; 5935658E21C4C89C CRC64;

Query Match 28.2%; Score 348.5; DB 2; Length 242;
Best Local Similarity 36.6%; Pred. No. 1.2e-20;
Matches 87; Conservative 37; Mismatches 77; Indels 37; Gaps 9;

Qy 8 NEKDLRKSELRN-ALSNLRQY---YNEKAITENKESDDPLENTLLFKGFTGHP 62
Db 17 NIKDL---SYAQGDIGVGNLRFYTKYDYIDLKGVTDKLPANQLE-----FSTG-- 64
Qy 63 WYNLDLVDSKDAFNKYGKKVLDYGAVYQCAAGTTPNKTACMYGVTLHDNNRLTEE 122
Db 65 -TNDLISESNWDEISRKFGKMDIFGIDYNGPC-----KTKYMGATL-SCGYLNSA 116
Qy 123 KVPINLMDGKQTVPIPIKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFG-GK-- 178
Db 117 RKIPINLMINGKHKTISTDKATNKLVTAQEIYDKLARYLOEENYIGHNNNGKXGYG 176
Qy 179 -----VQGLIVFHSSEGSTVSYDLFDAQGYPTTLRLRYDNKTINSENT-HIDL 228
Db 177 YKSKFYSGFNKGKVLFLHNDEKSFSDYDLFYTGDPVPSFLKIYEDNKTIISEKPHLDV 234

RESULT 30
Q6GFM9 PRELIMINARY; PRT; 242 AA.
ID Q6GFM9;
AC Q6GFM9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Enterotoxin.
OS OrderedLocustNames=SAR1919;
OC Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=282458;
RX NCI [1]
RP SEQUENCE FROM N.A.
```

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RX PubMed=15213324; DOI=10.1073/pnae.0402521101;
RA Houghton M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Entigen M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moulé S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
RL EMBL; BX571856; CAG40905.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bact_T_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_tox_OB.
DR Pfam; PF02876; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRI_TOXIN_
DR PROSITE; PS00278; STRAPH_STREP_TOXIN_2; 1.
KM Complete proteome.
SQ SEQUENCE 242 AA; 27950 MW; 5935658E21C4C89C CRC64;

Query Match 28.2%; Score 348.5; DB 2; Length 242;
Best Local Similarity 36.6%; Pred. No. 1.2e-20;
Matches 87; Conservative 37; Mismatches 77; Indels 37; Gaps 9;

Qy 8 NEKDLRKSELRN-ALSNLRQY---YNEKAITENKESDDPLENTLLFKGFTGHP 62
Db 17 NIKDL---SYAQGDIGVGNLRFYTKYDYIDLKGVTDKLPANQLE-----FSTG-- 64
Qy 63 WYNLDLVDSKDAFNKYGKKVLDYGAVYQCAAGTTPNKTACMYGVTLHDNNRLTEE 122
Db 65 -TNDLISESNWDEISRKFGKMDIFGIDYNGPC-----KTKYMGATL-SCGYLNSA 116
Qy 123 KVPINLMDGKQTVPIPIKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFG-GK-- 178
Db 117 RKIPINLMINGKHKTISTDKATNKLVTAQEIYDKLARYLOEENYIGHNNNGKXGYG 176
Qy 179 -----VQGLIVFHSSEGSTVSYDLFDAQGYPTTLRLRYDNKTINSENT-HIDL 228
Db 177 YKSKFYSGFNKGKVLFLHNDEKSFSDYDLFYTGDPVPSFLKIYEDNKTIISEKPHLDV 234

RESULT 31
Q8VVM1 PRELIMINARY; PRT; 225 AA.
ID Q8VVM1;
AC Q8VVM1;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 26, Last annotation update)
DE Exotoxin I.
GN Name=SpeI;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
NCBI_TaxID=1314;
RX NCI [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M1;
RA MEDLINE=21259899; PubMed=11359827;
RA Proft T., Arcus V.L., Handley V., Baker E.N., Fraser J.D.;
RT "Immunological and biochemical characterization of streptococcal
RT pyogenic exotoxins I and J (SPE-I and SPE-J) from Streptococcus
RT pyogenes.";
RL J. Immunol. 166:6711-6719(2001).
DR EMBL; AF438524; AAL31571.1; -.
DR HSSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
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Query Match	27.6%	Score 341.5	DB 2	Length 225
Best Local Similarity	34.8%	Pred. No. 4.2e-20		
Matches	77	Conservative	42	Mismatches 79; Indels 23; Gaps 6
QY	25	NLRQIYYNKAALTEKNSDDQPLENTLIPFGFFGFWYWN---	DLVLDSKQATNKYK	81
DB	8	NLRNLNLTSTDYDEYVKGKTNIEGPPSGSLFYKNI---	DYGNSSIEKLKVELNSVERKANFSS	63
QY	82	GKRDYLVGAYVGYOCAGCTPKNKTAOMYGVTLHDNNRLTEKRYPINLMIDG---	KQTTV	138
DB	64	GKRDYILFLEHSPPCNSNIKKNS---	YGGITLSDGNRI-DKNIRIVNIFIDVGQKSYT	119
QY	139	PIDVKYTSKKEVTVQVELDQARHYLHGKFGLY-----	NSDSFGKVGQGLIVFSS	189
DB	120	DISTVSTSKKEVTVIQLDLVKSRYVYLOKHFNFYIGFGVDVQGRSSRFOSGFEKGINII	FHLN	179
QY	190	EGSTVSYDLFDAQGYPPDTLLRIYDNKNTINSEMHIDLYL		230
DB	180	SGERISYVLPDTGHGDRSMLKRYSDNKTAVSDQLHIDIYL		220
RESULT 32				
085383		PRELIMINARY;	PRT;	242 AA.
ID	085383			
AC	085383			
DT	01-NOV-1998	(TREMBLrel. 08, Created)		
DT	01-NOV-1998	(TREMBLrel. 08, Last sequence update)		
DT	25-OCT-2004	(TREMBLrel. 28, Last annotation update)		
DE	Extracellular enterotoxin type I precursor (SEI).			
GN	Name=SEI; Synonyms=sei;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=FR1445;			
RX	MEDLINE=98298056; PubMed=9632603;			
RA	Munson S.H., Tremaine M.T., Betley M.J., Welch R.A.;			
RT	"Identification and characterization of staphylococcal enterotoxin			
RL	types G and I from Staphylococcus aureus.";			
RN	Infect. Immun. 66:3337-3348(1998).			
RP	[2]			
RC	SEQUENCE FROM N.A.			
RX	STRAIN=9A00322;			
RA	MEDLINE=20571956; PubMed=11123352;			
RT	Jarrat S., Peyrat M.A., Lim A., Tristan A., Bee M., Mougel C.,			
RL	Etienne J., Vandenesch F., Bonneville M., Lina G.;			
RT	"egc, a highly prevalent operon of enterotoxin gene, forms a putative			
RL	nursery of superantigens in Staphylococcus aureus.";			
RN	J. Immunol. 166:669-677(2001).			
DR	EMBL, AF064774; AAC2661.1; -			
DR	EMBL, AF285760; AAG36953.1; -			
DR	PIR, C89969; C89969.			
DR	HSSP, P13380; 1KTk.			
DR	GO; GO:0005576; C:extracellular; IEA.			
DR	GO; GO:0009405; P:pathogenesis; IEA.			
DR	InterPro, IPR008992; Bact_endocox.			
DR	InterPro, IPR006177; BactI_cox.			
DR	InterPro, IPR006123; Staph/Strep_toxin.			
DR	InterPro, IPR01123; Staph_toxin_1.			
DR	pfam, PF02876; Staph_stp_tox C; 1.			
DR	PRINTS, PR00279; BACTRLTOXIN			
DR	PROSITE, PS00278; STAPH_STREP_TOXIN 2; 1.			
DR	SEQUENCE	225 AA; 25654 MW; DB19367890ACDAF	CRC64;	

FT	CHINAL	1	24	Potential.
FT	SIGNAL	25	242	enterotoxin type I.
SO	SEQUENCE	242 AA;	27863 MW;	C5C8B4ACEB5414A8 CRC64;
Query Match		27.4%;	Score 339.5;	DB 2; Length 242;
Best Local Similarity		35.6%;	Pred. No. 6.7e-20;	
Matches		79;	Conservative 36;	Mismatches 74; Indels 33; Gaps 7;
Qy	LSNR:ROY----	YNEKAITENKESDDQFLNTLLFPGFPGHWNVDLVDLGSKDATN	78	
Db	30 VGNLRNFYTHKDYIDLGVTDKLPINANQLE-----FSTG---TNDLLSESNNWDEIS	79		
Qy	KYKKKATVDLGAAYGYGACAGTPEKTKACMGAGVTLHDNNRLTEKKYPIINLMIDGQTTV	138		
Db	80 KFKKKLDIFGIDYNGPC-----KSKYMWGATL-SCGYLNSARKIPINLWVNGDKHTI	132		
Qy	139 PIDKVTYSKKEVTVQVELDLQARHYLHGKFGLYNSDSFG-GK-----VORGILVF	186		
Db	133 STDKLTATNKLVTAQEIADVLRKRYLQREBNVNYGHANNNGKGEKGYKSKFYSGFNNGKVL	192		
Qy	187 HSEGSSTVSVDLPDAGQYEDTLRLRYNDKTTISENLHIDL	228		
Db	193 HLNNEKSFYSYDLFYTGDLPLVPSFKIYEDNNKIIESEKPHLDV	234		
RESULT 33				
Q7A205				
Q7A205	PRELIMINARY;	PRT;	242 AA.	
AC	Q7A205;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	Extracellulular enterotoxin type I.			
GN	Name=sei; OrderedLocustNames=SAV1828;			
OS	Staphylococcus aureus (strain Mu50 / ATCC 706069).			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=158878;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;			
RA	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,			
RA	Cui L., Oguchi A., Aoki K.-I., Nagai Y., Itoh T.,			
RA	Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hasegawa A.,			
RA	Mizutani M., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,			
RA	Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,			
RA	Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,			
RA	Hattori M., Ogasawara N., Hayashi H., Hiratsuka K.;			
RT	"Whole genome sequencing of methicillin-resistant Staphylococcus			
RT	aureus."			
RL	Lancet 357:1225-1240(2001).			
DR	EMBL; AP003363; BAB57990.1; "			
DR	GO; GO:0005576; C:extracellular; IEA.			
DR	GO; GO:0004905; P:pathogenesis; IEA.			
DR	InterPro; IPR006992; Bact_endotox.			
DR	InterPro; IPR006177; BactI_tox.			
DR	InterPro; IPR006123; Staph/Strep_toxin.			
DR	InterPro; IPR006173; Staph_tox_OB.			
DR	Pfam; PF01123; Staph_Strep_toxin; 1.			
DR	Pfam; PF02876; Staph_Strep_tox_C; 1.			
DR	PRINTS; PR00279; BACTRITOXIN.			
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.			
KW	Complete proteome.			
SEQ	SEQUENCE 242 AA; 27863 MW; C5C8B4ACEB5414A8 CRC64;			
Query Match		27.4%;	Score 339.5;	DB 2; Length 242;
Best Local Similarity		35.6%;	Pred. No. 6.7e-20;	
Matches		79;	Conservative 36;	Mismatches 74; Indels 33; Gaps 7;
Qy	LSNR:ROY----	YNEKAITENKESDDQFLNTLLFPGFPGHWNVDLVDLGSKDATN	78	
Db	30 VGNLRNFYTHKDYIDLGVTDKLPINANQLE-----FSTG---TNDLLSESNNWDEIS	79		
Qy	KYKKKATVDLGAAYGYGACAGTPEKTKACMGAGVTLHDNNRLTEKKYPIINLMIDGQTTV	138		
Db	80 KFKKKLDIFGIDYNGPC-----KSKYMWGATL-SCGYLNSARKIPINLWVNGDKHTI	132		
Qy	139 PIDKVTYSKKEVTVQVELDLQARHYLHGKFGLYNSDSFG-GK-----VORGILVF	186		
Db	133 STDKLTATNKLVTAQEIADVLRKRYLQREBNVNYGHANNNGKGEKGYKSKFYSGFNNGKVL	192		
Qy	187 HSEGSSTVSVDLPDAGQYEDTLRLRYNDKTTISENLHIDL	228		
Db	193 HLNNEKSFYSYDLFYTGDLPLVPSFKIYEDNNKIIESEKPHLDV	234		
RESULT 33				
Q7A205				
Q7A205	PRELIMINARY;	PRT;	242 AA.	
AC	Q7A205;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	Extracellulular enterotoxin type I.			
GN	Name=sei; OrderedLocustNames=SAV1828;			
OS	Staphylococcus aureus (strain Mu50 / ATCC 706069).			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=158878;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;			
RA	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,			
RA	Cui L., Oguchi A., Aoki K.-I., Nagai Y., Itoh T.,			
RA	Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hasegawa A.,			

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Db      80 KFKGKGLDIFGIDYNGPC-----RSKYMGGATLL-SCQYLSNARKIPINLMWNGKHKT 132
Oy      139 PIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFG-GK-----VQRLIVF 186
Db      133 STDKATNKKLVTAQEDIVKLRVYQOEENYIGHNNTGKGEYKSKFSPFNNKYLIF 192
Oy      187 HSSGGSIVSYDLFDAQGYPTDLLRIYRDNKTINSENLHIDL 228
Db      193 HLNNEKSFYSYDLFYTGDLFPVSFLKIYEDNKTIIESEKPHLDV 234
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RESULT 34

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O7A4W8 PRELIMINARY; PRT; 242 AA.
ID O7A4W8
AC O7A4W8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Extracelluluar enterotoxin type I.
GN Name=sel; OrderedlocusNames=SA1646;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_Taxid=158879;
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SEQUENCE FROM N.A.
EMBL; AP003364; BAB58170.1; -.
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuuchi J.,
RA Katsuhira M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratsugu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003364; BAB58170.1; -.
DR GO; GO:0005576; C:extracelluluar; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactr_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph/Strep_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN_
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 242 AA; 27863 MW; C5C8BAACE5414A8 CRC64;
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Query Match 27.4%; Score 339.5; DB 2; Length 242;
Best Local Similarity 35.6%; Pred. No. 6.7e-20;
Matches 79; Conservative 36; Mismatches 74; Indels 33; Gaps 7;
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Oy      23 LSNLRQIY----YNNKAIITENKESDDQFLNTLLFKGFTGHPWYNDL-LVLDGSKDATN 78
Db      30 VGNLNFPTTKHDYIDLKGVTDKNLPIANGL-----FSTG---TNDLISSNMDEIS 79
Oy      79 KYGKKVLDYGAYYGYQACGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTV 138
Db      80 KFKGKGLDIFGIDYNGPC-----RSKYMGGATLL-SCQYLSNARKIPINLMWNGKHKT 132
Oy      139 PIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFG-GK-----VQRLIVF 186
Db      133 STDKATNKKLVTAQEDIVKLRVYQOEENYIGHNNTGKGEYKSKFSPFNNKYLIF 192
Oy      187 HSSGGSIVSYDLFDAQGYPTDLLRIYRDNKTINSENLHIDL 228
Db      193 HLNNEKSFYSYDLFYTGDLFPVSFLKIYEDNKTIIESEKPHLDV 234
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RESULT 35

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O7A2N9 PRELIMINARY; PRT; 240 AA.
ID O7A2N9
AC O7A2N9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Extracelluluar enterotoxin L.
GN Name=sel; OrderedlocusNames=SAV2008;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_Taxid=158878;
```

```
SEQUENCE FROM N.A.
EMBL; AP003364; BAB58170.1; -.
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuuchi J.,
RA Katsuhira M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratsugu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003364; BAB58170.1; -.
DR HSSP; P13380; IAN8.
DR GO; GO:0005576; C:extracelluluar; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactr_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph/Strep_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN_
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 240 AA; 27496 MW; F40D62DA73197881 CRC64;
```

```
Query Match 27.2%; Score 337; DB 2; Length 240;
Best Local Similarity 35.3%; Pred. No. 1.1e-19;
Matches 78; Conservative 37; Mismatches 72; Indels 34; Gaps 6;
```

```
Oy      25 NLRQIY----YNNKAIITENKESDDQFLNTLLFKGFTGHPWYND-LVLDGSKDATNK 79
Db      32 NLRNFTTKRYEYNLKNVNDKNSPESHRL-----YSKNDTIYAFEDNEYITS 80
Oy      80 YGKKVLDYGAYYGYQACGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTV 139
Db      81 LKGNKVDVFGISYKY-----GNSRT--LYGVTVKAKNNKLDSPRIIPINLIINGHQT 134
Oy      140 IDKVTSKKEVTVQELDLQARHYLHGKGLY-----NSDSGKGVQRLIYFH 187
Db      135 TKSIVTDKQWVTAQEDIVKLRVYQOEENYIGHNNTGKGEYKSKFSPFNNKYLIF 194
Oy      188 SSEGGSIVSYDLFDAQGYPTDLLRIYRDNKTINSENLHIDL 228
Db      195 MWDGSNFSYDLFYTGGLPVSFLKIYKDKNTVDSIQFHLVD 235
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RESULT 36

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O7A4K9 PRELIMINARY; PRT; 240 AA.
ID O7A4K9
AC O7A4K9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Extracelluluar enterotoxin L.
GN Name=sel; OrderedlocusNames=SA1816;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
```

OK NCBI_TaxID=158879;
 RP [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian Y.-Q., Ito T.,
 RA Katsumori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani-U Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshida K., Hiramatsu K.,
 RA Hatooli M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*."
 RT Lancel 359.1819-1827(2002).
 RU EMBL, AP004135; BAB94625.1; -.
 DR HSSP; P1380; 1AB0.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bactl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph/Strep_tox.
 DR Pfam; PF01123; Staph_strep_toxin; 1.
 DR Pfam; PF02876; Staph_strep_toxin; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR Complete proteome.
 SQ SEQUENCE 240 AA; 27496 MW; F40D62DA73197881 CRC64;

Query Match 27.2%; Score 337; DB 2; Length 240;
 Best Local Similarity 35.3%; Pred. No. 1.1e-19; Indels 34; Gaps 6;
 Matches 78; Conservative 37; Mismatches 72;
 QY 25 NRQY-----YYNEKAITENKESDDQFLENTLLFKGFFTHPWPYND-LIVDLGSKDATNK 79
 DB 32 NLRNFTTKETVNLKXVNDKNSPESHRL-----YKXNDTLVAFEDNEVITSD 80
 QY 80 YGKKVLDYGAAYGYQCAAGTPNKTCMYGVTLLHNNRLTEKKVPINLMIDGKQTV 139
 DB 81 LKGNVDVFGISYK-----GSNSRT--YGGVTKAENNLDSPPRIIPINLIINGKHQTV 134
 QY 140 IDKVTSKKQVTVQELDLQARHLYLHGKFGLY-----NDSFGGKQVGLIVH 187
 DB 135 TKSVSSTDKKQVTVQELDLQARHLYLHGKFGLY-----NDSFGGKQVGLIVH 194
 QY 188 SSEGSTVSVDLPDAQGYPTLLRIYRDNKTINSENLHIDL 228
 DB 195 MNDGSNFSYDLPFTYGYGLPESFLIKYDKNTKVDSTQPHLDV 235

RESULT 37
 ID 09FOL7 PRELIMINARY; PRT; 240 AA.
 AC 09FOL7;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Sel.
 GN Name=sel.
 OS *Staphylococcus aureus*.
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2056666; PubMed=11114901; DOI=10.1128/JB.183.1.63-70.2001;
 RA Fitzgerald J.R., Monday S.R., Foster T.J., Bonach G.A., Hattigan P.J.,
 RA Meaney W.J., Smyth C.J.;
 RT "Characterization of a putative pathogenicity island from bovine
 RT *Staphylococcus aureus* encoding multiple superantigens."
 RT J. Bacteriol. 183:63-70(2001).
 DR EMBL, AF217235; AAG29598.1; -.

DR PIR; G89991; G89991.
 DR HSSP; Q9R005; 1ET6.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bactl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph/Strep_tox.
 DR Pfam; PF01123; Staph_strep_toxin; 1.
 DR Pfam; PF02876; Staph_strep_toxin; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR SEQUENCE 240 AA; 27496 MW; F40D62DA73197881 CRC64;

Query Match 27.2%; Score 337; DB 2; Length 240;
 Best Local Similarity 35.3%; Pred. No. 1.1e-19; Indels 34; Gaps 6;
 Matches 78; Conservative 37; Mismatches 72;
 QY 25 NRQY-----YYNEKAITENKESDDQFLENTLLFKGFFTHPWPYND-LIVDLGSKDATNK 79
 DB 32 NLRNFTTKETVNLKXVNDKNSPESHRL-----YKXNDTLVAFEDNEVITSD 80
 QY 80 YGKKVLDYGAAYGYQCAAGTPNKTCMYGVTLLHNNRLTEKKVPINLMIDGKQTV 139
 DB 81 LKGNVDVFGISYK-----GSNSRT--YGGVTKAENNLDSPPRIIPINLIINGKHQTV 134
 QY 140 IDKVTSKKQVTVQELDLQARHLYLHGKFGLY-----NDSFGGKQVGLIVH 187
 DB 135 TKSVSSTDKKQVTVQELDLQARHLYLHGKFGLY-----NDSFGGKQVGLIVH 194
 QY 188 SSEGSTVSVDLPDAQGYPTLLRIYRDNKTINSENLHIDL 228
 DB 195 MNDGSNFSYDLPFTYGYGLPESFLIKYDKNTKVDSTQPHLDV 235

RESULT 38
 ID 08XKJ5 PRELIMINARY; PRT; 240 AA.
 AC 08XKJ5;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2004 (TReMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Extracellular enterotoxin L.
 GN Name=sel2; Ordered locus names=MM0760;
 OS *Staphylococcus aureus* (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08773-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwano M., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA."
 RT Lancet 359.1819-1827(2002).
 RU EMBL, AP004824; BAB94625.1; -.
 DR HSSP; Q9R005; 1ET6.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bactl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph/Strep_tox.
 DR Pfam; PF01123; Staph_strep_toxin; 1.
 DR Pfam; PF02876; Staph_strep_toxin; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

KW Complete proteome. 27478 MW; 85CD62DAY31C3D95 CRC64;
SQ SEQUENCE 240 AA; 27478 MW; 85CD62DAY31C3D95 CRC64;
Query Match 27.1%; Score 336; DB 2; Length 240;
Best Local Similarity 35.3%; Pred. No. 1.3e-19;
Matches 78; Conservative 37; Mismatches 72; Indels 34; Gaps 6;
QY 25 NLRLQIY---YNEKAITENKESDDQLENTLLFKGFTGHPWYND-LLVDIGSKDATNK 79
DB 32 NLRLNYTKKEYNLKGVNDKNSPESHRL-----YSKNDTLAEFDNEEYITSD 80
QY 80 YKGVKVDLYGAYVYQACAGTPTNKACMYGVTLLHNNRLTEKKVPIINLMIDGKQTVF 139
DB 81 LKGVKVDVFGISYK---GNSRT--LYGVTKAKNNKLDSPRIPIINLILINGKHQTVT 134
QY 140 IDKVYTSKKEVTVQELDLQARHYLHGKFGLY-----NSDSFGKVGQGLIVFH 187
DB 135 TKSVSTDKKMTAQTQIDVTKRYQLQDEFNITGHNTGKCKEYGTSGSFGRKGSVVFH 194
QY 188 SSEGSTVSVDLFDAGQGYPTTLRLRYDNKNTINSENHLIDL 228
DB 195 INDGSNFSYDLYFTYTGGLPESFLIKYKDKTKVDSTQFHLDV 235

RESULT 39
Q8RR75 PRELIMINARY; PRT; 218 AA.
AC Q8RR75; 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Enterotoxin I (Fragment).
GN Name=sei;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
RN [1]
RX MEDLINE=21871379; PubMed=11880405;
RA Omeo K., Ishikawa M., Shimoda Y., Hu D.L., Ueda S., Shingawa K.;
RT "Detection of seg, seh, and sei genes in Staphylococcus aureus
isolates and determination of the enterotoxin productivities of S.
aureus isolates harboring seg, seh, or sei genes";
RL J. Clin. Microbiol. 40:857-862(2002).
DR HSBP; P13380; 1XTK.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR Pfam; PF01123; Staph/Strep_toxin.
DR Pfam; PF02876; Staph/Strep_toxin; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 218 AA; 24909 MW; 1017728FB71BF662 CRC64;

Query Match 27.1%; Score 335.5; DB 2; Length 218;
Best Local Similarity 35.1%; Pred. No. 1.3e-19;
Matches 78; Conservative 37; Mismatches 74; Indels 33; Gaps 7;
QY 23 LSNLRQIY---YNEKAITENKESDDQLENTLLFKGFTGHPWYNDLLVDIGSKDATN 78
DB 6 VGNLNFYTKHDYIDLKGVTDKPLPLANQLE-----FSTG---TNDLISSENWDEIS 55
QY 79 KYKGVKVDLYGAYVYQACAGTPTNKACMYGVTLLHNNRLTEKKVPIINLMIDGKQTV 138
DB 56 KFGKVKLDLIFGIDYNGPC-----SKYMFSGATL--SGQYLSARKIPINLWVNGKHKT 108
QY 139 PIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFG-----VQGLIVF 186
DB 109 STDKTIATNKGLVTADRIDVTKRLRYLQDEFNITGHNTGKCKEYGTSGSFGRKGSVVFH 168

QY 187 HSSEGSTVSVDLFDAGQGYPTTLRLRYDNKNTINSENHLIDL 228
DB 169 HNNKESFSYDLYFTYTGGLPVSFLIKYEDNKIIESEKPHLDV 210

RESULT 40
Q9L921 PRELIMINARY; PRT; 225 AA.
AC Q9L921; 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE 25.7 kDa protein.
OS Streptococcus equi.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
NCBI_TaxID=1336;
RN [1]
RX STRAIN=CF32;
RX MEDLINE=21671707; PubMed=11812213; DOI=10.1006/ypat.2001.0482;
RA Artinushin S.C., Timoney J.F., Sheoran A.S., Muthupalan S.K.;
RT "Characterization and immunogenicity of pyrogenic mitogens SepH and
RT SepE-I of Streptococcus equi";
RL Microb. Pathog. 32:71-85(2002).
DR HSBP; AF186180; AAF72808.1; --.
DR HSBP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph/Strep_tox.
DR Pfam; PF01123; Staph/Strep_toxin; 1.
DR Pfam; PF02876; Staph/Strep_toxin; 1.
DR PRINTS; PR00279; BACTRTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 225 AA; 25684 MW; EB43D47B26FB9F89 CRC64;

Query Match 27.1%; Score 335.5; DB 2; Length 225;
Best Local Similarity 34.4%; Pred. No. 1.3e-19;
Matches 76; Conservative 42; Mismatches 80; Indels 23; Gaps 6;
QY 25 NLRLQIYNEKAITENKESDDQLENTLLFKGFTGHPWYND--DLVDIGSKDATNKYK 81
DB 8 NLRLNYSTYDLYFTYTGGLPVSFLIKYEDNKIIESEKPHLDV 210
QY 82 GKVVDLYGAYVYQACAGTPTNKACMYGVTLLHNNRLTEKKVPIINLMIDG--KQTV 138
DB 64 GKVVDLYGAYVYQACAGTPTNKACMYGVTLLHNNRLTEKKVPIINLMIDG--KQTV 119
QY 139 PIDKVTSSKEVTVQELDLQARHYLHGKFGLY-----NSDSFGKVGQGLIVFH 189
DB 120 DLSVSTDKKEVTVQELDLQARHYLHGKFGLY-----NSDSFGKVGQGLIVFH 179
QY 190 EGSSTVSVDLFDAGQGYPTTLRLRYDNKNTINSENHLIDL 230
DB 180 SGERISYVLPDGHGDRSMKLYSDNKTAVSDQHLHIDYL 220

RESULT 41
Q99Z21 PRELIMINARY; PRT; 225 AA.
AC Q99Z21; 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Streptococcal exotoxin I.
GN Name=sepi; OrderedLocName=SPY1007;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLOTXIN-
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KM Complete proteome.
SQ SEQUENCE 239 AA; 27370 MW; 5F29665125705600 CRC64;

Query Match 25.8%; Score 320; DB 2; Length 239;
Best Local Similarity 33.0%; Pred. No. 2.7e-18;
Matches 72; Conservative 40; Mismatches 78; Indels 28; Gaps 6;

QY 25 NLRLQIYYNEKAIYENK--ESDDQFLENTLLFKGFPTGHPWYNDLLVLDGSDATANKYK 82
DB 28 NLRLN--YVGSYPIDHOSINPENNLISHQLVES-----MDNSTYTAEPKXVDVKKFKN 79
QY 83 KKVLDYGAIVYGQAGTGNPKTACMGVTLHDNNRLTEKKVPINLMIDGKOTVPIDK 142
DB 80 HAVDVGISYSGYCL-----KKKTYGGVTL-AGDYLEKSRRIPIINLWNGEHQITISDK 133
QY 143 VKTSKEVTVOELDQARHYLHGKFGLY-----NSDFGKVGQGLIVFHSSE 190
DB 134 VSTNKKVLTAGIEDTKLARIYQEEYNIYGFNDTNKGRNYGKSKSGFNKGLIFHLND 193
QY 191 GSTVSYDLFPAQGGYPTDLRLRIYRDNKTINSENHIDL 228
DB 194 GSSFSYDLFDYGTGQAESFLKIYNDNKTIVETEKFLHDV 231

RESULT 44

Q8NVM3 PRELIMINARY; PRT; 242 AA.

AC Q8NVM3;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Staphylococcal enterotoxin Seg.
GN Name=seg2; OrderedLocustNames=MM1937;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RA [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RL MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hirumatsu K.,
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR HSSP; P13380; IKTK.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR008375; Staph_exotoxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLOTXIN-
DR PROSITE; PR01800; STAPHSTREP_TOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KM Complete proteome.
SQ SEQUENCE 242 AA; 28139 MW; FFC089BBOE7A3BF5 CRC64;

Query Match 25.8%; Score 319.5; DB 2; Length 242;
Best Local Similarity 33.8%; Pred. No. 3e-18; Indels 43; Gaps 8;
Matches 76; Conservative 35; Mismatches 71;

QY 25 NLRLQIYYNEK--AITENKESDDQFLENTLLFKGFPTGHPWYNDLLVLDGSDATANKY 80
DB 32 NLRLNRYANYQPEKIQGVSSGNFSTSHOLE---YIDGKTYLTSQPH-----NEY 76
QY 81 KGK-----KVLDYGAIVYGQAGTGNPKTACMGVTLHDNNRLTEKKVPINLMIDGK 135
DB 77 EAKRLKHKVDIFGISYGLC-----NTKMYGQITLANON-LDKPRNIPINLMVNGKQ 129
QY 136 TTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYN-----SDSFGKVGQGL 183
DB 130 NTISDVKSTQKKEVTVAQIEDIKLRKYLQNEYNINYGFKTKGQEGYKSKFNSGFNGK 189
QY 184 IVFHSSEGSCTSYDLFPAQGGYPTDLRLRIYRDNKTINSENHIDL 228
DB 190 ITFHLNNEPSFTYDLFYGTGQAESFLKIYNDNKTIDAENFHLDV 234

RESULT 45

Q6G7U1 PRELIMINARY; PRT; 242 AA.

AC Q6G7U1;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin.
GN OrderedLocustNames=SAS1920;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=262459;
RA [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnae.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.,
RT "Complete genomes of two clinical Staphylococcus aureus strains:
evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571857; CAG34727.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR008375; Staph_exotoxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLOTXIN.
DR PROSITE; PR01800; STAPHSTREP_TOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KM Complete proteome.
SQ SEQUENCE 242 AA; 28139 MW; FFC089BBOE7A3BF5 CRC64;

Query Match 25.8%; Score 319.5; DB 2; Length 242;
Best Local Similarity 33.8%; Pred. No. 3e-18;
Matches 76; Conservative 35; Mismatches 71; Indels 43; Gaps 8;

QY 25 NLRLQIYYNEK--AITENKESDDQFLENTLLFKGFPTGHPWYNDLLVLDGSDATANKY 80
DB 32 NLRLNRYANYQPEKIQGVSSGNFSTSHOLE---YIDGKTYLTSQPH-----NEY 76
QY 81 KGK-----KVLDYGAIVYGQAGTGNPKTACMGVTLHDNNRLTEKKVPINLMIDGK 135
DB 77 EAKRLKHKVDIFGISYGLC-----NTKMYGQITLANON-LDKPRNIPINLMVNGKQ 129

QY 136 TTVPIDKVTSSKEVTVQELDQARHYLHGKRGFLYN-----SDSPGKVVQRL 183
 DB 130 NTISTDKVSTQKEVTAQAEIDIKRLKYLQNEVNIYGFNKKQGEYGYSKFNPGK 189
 QY 184 IVFHSSEGSTVSYDLFDAGQGYPTLLRIYRNKNTINSENHIDL 228
 DB 190 ITFHLNNEPSFTYDLFYGTGQAESFLKIYNDKNTIDANFHLDV 234

RESULT 46

Q8VLM7 PRELIMINARY; PRT; 256 AA.
 ID 08VLM7
 AC 08VLM7
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Staphylococcal enterotoxin Q.
 GN Name=entQ;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BN4282;
 RX MEDLINE=98385824; PubMed=9720870;
 RA Lindsay J.A., Kuzin A., Ross H.F., Kurepina N., Novick R.P.;
 RT "The gene for toxic shock toxin is carried by a family of mobile
 pathogenicity islands in Staphylococcus aureus."
 RL Mol. Microbiol. 29:527-543 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BN4282;
 RA Barry P.C., Novick R.P.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U93688; AAL67620.1; -.
 DR HSSP; P13380; 1KTK.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PRINTS; PR01800; STAPHEXOTOXN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 SQ SEQUENCE 256 AA; 29794 MW; 9E2F13790823A7DF CRC64;

Query Match 25.7%; Score 318.5; DB 2; Length 256;
 Best Local Similarity 33.8%; Pred. No. 3, 8e-18;
 Matches 76; Conservative 35; Mismatches 71; Indels 43; Gaps 8;

QY 25 NLRQIY--YYNEK--AITENKESDDQFLENTLLFKGFFGHFWYNDLLVDLSKDATNKY 80
 DB 46 NLRNFYANPEPELQGVSSGNFSTSHQLR---YIDGKYLTYSGFH-----NEV 90
 QY 81 KKG-----KYDLYGAYGYQACGTPNKTAQMGVTLIDNNRLLTEKKVPINLWIDGKQ 135
 DB 91 EAKRLDKHKVDLFGISYSGLC-----NTKMYGGITLANON--LDKPRNIPINLWNGKQ 143
 QY 136 TTVPIDKVTSSKEVTVQELDQARHYLHGKRGFLYN-----SDSPGKVVQRL 183
 DB 144 NTISTDKVSTQKEVTAQAEIDIKRLKYLQNEVNIYGFNKKQGEYGYSKFNPGK 203
 QY 184 IVFHSSEGSTVSYDLFDAGQGYPTLLRIYRNKNTINSENHIDL 228
 DB 204 ITFHLNNEPSFTYDLFYGTGQAESFLKIYNDKNTIDANFHLDV 248

RESULT 47
 Q93CC6 PRELIMINARY; PRT; 242 AA.
 ID 093CC6
 AC 093CC6
 DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

GN Name=seq;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COL;
 RX MEDLINE=21935388; PubMed=11821418; DOI=10.1074/jbc.M11661200; V.,
 RA Yarwood J.M., McCormick J.K., Paustian M.L., Orwin P.M., Kapur V.,
 RT "Characterization and expression analysis of Staphylococcus aureus
 pathogenicity island 3. Implications for the evolution of
 staphylococcal pathogenicity islands."
 RL J. Biol. Chem. 277:13138-13147 (2002).
 DR EMBL; AF410775; AAL04146.1; -.
 DR HSSP; P13380; 1KTK.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bactl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR008375; Staph_exotoxin.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PRINTS; PR01800; STAPHEXOTOXN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 SQ SEQUENCE 242 AA; 28184 MW; F6E8FDAF6C30D85 CRC64;

Query Match 25.6%; Score 316.5; DB 2; Length 242;
 Best Local Similarity 33.8%; Pred. No. 5, 2e-18;
 Matches 76; Conservative 35; Mismatches 71; Indels 43; Gaps 8;

QY 25 NLRQIY--YYNEK--AITENKESDDQFLENTLLFKGFFGHFWYNDLLVDLSKDATNKY 80
 DB 32 NLRNFYANPEPELQGVSSGNFSTSHQLR---YIDGKYLTYSGFH-----NEV 76
 QY 81 KKG-----KYDLYGAYGYQACGTPNKTAQMGVTLIDNNRLLTEKKVPINLWIDGKQ 135
 DB 77 EAKRLDKHKVDLFGISYSGLC-----NTKMYGGITLANON--LDKPRNIPINLWNGKQ 129
 QY 136 TTVPIDKVTSSKEVTVQELDQARHYLHGKRGFLYN-----SDSPGKVVQRL 183
 DB 130 NTISTDKVSTQKEVTAQAEIDIKRLKYLQNEVNIYGFNKKQGEYGYSKFNPGK 189
 QY 184 IVFHSSEGSTVSYDLFDAGQGYPTLLRIYRNKNTINSENHIDL 228
 DB 190 ITFHLNNEPSFTYDLFYGTGQAESFLKIYNDKNTIDANFHLDV 234

RESULT 48
 Q9E2M7 PRELIMINARY; PRT; 239 AA.
 ID 09E2M7
 AC 09E2M7
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE SEM.
 GN Name=sem;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A900322;
 RX MEDLINE=20571956; PubMed=11123352;
 RA Jarraud S., Peyrat M.A., Lim A., Tristan A., Bee M., Mougel C.,

RA Etienne J., Vandenesch F., Bonneville M., Iina G.,
RT "egc", a highly prevalent operon of enterotoxin gene, forms a putative
nucleus of superantigen in *Staphylococcus aureus*.",
RL J. Immunol. 166:669-677(2001).
DR EMBL: AF285760; AAC36952.1; -.
DR HSBP: Q9RQ05; 1E76.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bactl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006173; Staph_tox_0B.
DR Pfam: PF01123; Staph_Strep_toxin_1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN-
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 239 AA; 27371 MW; 69240BE23C44028A CRC64;

Query Match 25.5%; Score 316; DB 2; Length 239;
Best Local Similarity 32.6%; Pred. No. 5.7e-18;
Matches 71; Conservative 41; Mismatches 78; Indels 28; Gaps 6;

QY 25 NLRLQIYYNEKAITENK--ESDDQFLENTLLFKGFFTGHPWNTDLLVDLGSKDATNKYKG 82
DB 28 NLRL--YGYSPFIEDHQSINPENHLSHQLVFS-----MDNSTYAEFKVNDVKEFKN 79
QY 83 KKVLDYGAAYGYQCAGTPTNCTACMYGVTLDHNNRLTEKKVPINLMDGKQTTVPIDK 142
DB 80 HAVDVYGLSYSGYCL-----KKKYTYGGVTL-AGVYLEKSRRIPIINLVNGEHQIISIDK 133
QY 143 VKTSKEVTVQELDIQARHYLHGKFGLY-----NSDFGKVGQRLIVFHSSE 190
DB 134 VSTNKKLVTAQIEDIKLRRLYQEEFNIVGFNDTNKGRVYGNKSPSGFNAGKILFHLND 193
QY 191 GSTVSYDLFDAGQYPTLLRIYRNKNTINSNLHIDL 228
DB 194 GSSPSYDLFDGTGQAFSLFKIYNDKNTVEKEFHLDV 231

RESULT 49

ID Q711S9 PRELIMINARY; PRT; 86 AA.
AC Q711S9;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Putative enterotoxin (Fragment).
OS *Staphylococcus intermedius*.
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
OX NCBI_TaxID=1285;
RN [1]
RP SEQUENCE FROM N.A.
RA Becker K.;
RL Thesis (2001), Department of Institute of Medical Microbiology,
University of Munster, Munster, Germany.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
FT NON TER 86
SQ SEQUENCE 86 AA; 9877 MW; 21C191E65BAF72AC CRC64;

Query Match 25.2%; Score 312; DB 2; Length 86;
Best Local Similarity 66.3%; Pred. No. 3.5e-18;
Matches 57; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

QY 127 INLWMDGQTTVPIDKVKTSKEVTVQELDIQARHYLHGKFGLYNSDSFGGVQRLIVF 186
DB 1 VNLWMDGQTTVPIDKVKTSKEVTVQELDIQARHYLHGKFGLYNSDSFGGVQRLIVF 60

QY 187 HSSGQTVSYDLFDAGQYPTLLRI 212
DB 61 ETSRKHSAVDLYAAEKGADTIIRI 86

RESULT 50

ID Q8NVW2 PRELIMINARY; PRT; 242 AA.
AC Q8NVW2;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE *Staphylococcus enterotoxin* Sek.
GN Name=sek2; OrderedLocustNames=MM1938;
OS *Staphylococcus aureus* (strain MW2).
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.,
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RT Lancet 359:1819-1827(2002).
DR EMBL: AP004828; BAB95803.1; -.
DR HSBP: P13380; 1KTK.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bactl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006173; Staph_tox_0B.
DR Pfam: PF01123; Staph_Strep_toxin_1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 242 AA; 27848 MW; FC377CB4C9BBB4E3 CRC64;

Query Match 25.0%; Score 310; DB 2; Length 242;
Best Local Similarity 33.2%; Pred. No. 1.8e-17;
Matches 74; Conservative 39; Mismatches 76; Indels 34; Gaps 9;

QY 23 LSNLRQIY----YNEKAITENKESDDQFLENTLLFKGFFTGHPWNTDLLVDLGSKDXTN 78
DB 29 IDNLRNFYTKDFINLKVNDKDN---DTPINQLOP-----SNSY-DLISESKDPNFKFS 78
QY 79 KYGKKVLDYGAAYGYQCAGTPTNCTACMYGVTLDHNNRLTEKKVPINLMDGKQTTV 138
DB 79 NFKGKKLDVFGISYNGC-----NTKYTYGGITR-TREYLDKRRNIPINLVNGEHQIISIDK 131
QY 139 PIDKVKTSKEVTVQELDIQARHYLHGKFGLY-----NSDFGKVGQRLIVFHSSE 186
DB 132 STNKKVSTNKKVTVQELDIQARHYLHGKFGLY-----NSDFGKVGQRLIVFHSSE 191
QY 187 HSSGQTVSYDLFDAGQYPTLLRIYRNKNTINSNLHIDL 228
DB 192 HLNNDTFSYDLFDGTGDDLPKSPFKIYEDKNTVESEKFLHDV 234

RESULT 51

ID Q6G7U0 PRELIMINARY; PRT; 242 AA.
AC Q6G7U0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin.
GN OrderedLocustNames=SAS1921;
OS *Staphylococcus aureus* (strain MSSA476).

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101.
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corbin A., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 DR EMBL: BX571857; CAG43728.1;
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR006177; Bact_endotox.
 DR InterPro: IPR006177; Bact_tox.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF01123; Staph_Strep_toxin; 1.
 DR Pfam: PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS: PR00279; BACTRLTOXIN_1
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR Complete proteome.
 SQ SEQUENCE 242 AA; 27848 MW; FC377CB4C9BB4E3 CRC64;
 Query Match 25.0%; Score 310; DB 2; Length 242;
 Best Local Similarity 33.2%; Pred. No. 1.8e-17;
 Matches 74; Conservative 39; Mismatches 76; Indels 34; Gaps 9;
 QY 23 LSNLRQIY----YNEKAITENKSDQFLNTLFGKFTGHPWYNDLLVDGSKDATN 78
 DB 29 IONLRNFYRKQPINLKDQVND---DTPIANQLQF-----SNESY-DLISEKDPNKKS 78
 QY 79 KYKGGKVDLYGAYYGYQACAGTNTKACMGVGLTLDNNRLTEKKVPIPLMWIDGQITV 138
 DB 79 NFGKKGLDVPFGISYNQC-----NTRYIGGITTA-TNEYLDPRNIPIMWINGNHKTI 131
 QY 139 PIDKVTSSKEVTVQELDLQARHYLHGKFGLY-----NSDSFGK-----VQGLIVF 186
 DB 132 STNKVSTNKKVTAQGLDIDLRRLQLEBNIVYGHNGTKGGEYKSKFVSGNIGKATF 191
 QY 187 HSESGSTVSYDLF-DAQGYPTLLRIYRDNKTINSENHIDL 228
 DB 192 HANNDTFPSYDLFYTGDDGLPKSPFKIYEDNKTVESKFFHLDV 234
 RESULT 52
 Q6R2F8 PRELIMINARY; PRT; 163 AA.
 AC 06R2F8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 OS Enterotoxin Q (Fragment).
 OS Staphylococcus aureus subsp. aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=46170;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 27664;
 RX PubMed=15131181;
 RA Sergeev N., Volokhov D., Chizhikov V., Rasooly A.;
 RT "Simultaneous analysis of multiple Staphylococcal enterotoxin genes by
 RT an oligonucleotide microarray assay.";
 RL J. Clin. Microbiol. 42:2134-2143(2004).
 DR EMBL: AY518389; AAR9637.1; -
 DR HSSP: P13380; 1AN8.

DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR008992; Bact_endotox.
 DR InterPro: IPR006177; Bact_tox.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006126; Staph/Strep_tox.
 DR InterPro: IPR008375; Staph_exotoxin.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF01123; Staph_Strep_toxin; 1.
 DR Pfam: PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS: PR00279; BACTRLTOXIN_1
 DR PRINTS: PR01800; STAPHSTREP_TOXIN_1; UNKNOWN_1.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1;
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR NON TER 1 1
 FT 163 163
 SQ SEQUENCE 163 AA; 19011 MW; C4F7B02D47D600F3 CRC64;
 Query Match 25.0%; Score 309; DB 2; Length 163;
 Best Local Similarity 37.7%; Pred. No. 1.3e-17;
 Matches 63; Conservative 27; Mismatches 53; Indels 24; Gaps 4;
 QY 78 NKYKKG-----KVDLYGAYYGYQACAGTNTKACMGVGLTLDNNRLTEKKVPIPLMWID 132
 DB 4 NNEYEARQLDKHAKVDLFGISYSGLC-----NTRYIGGITLANON-LDKPNIPIPLMWYN 56
 QY 133 GKQTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYN-----SDSFGKQVQ 180
 DB 57 GKQNTISTKVKSTQKEVTAQGLDIDLRRLQLEBNIVYGHNGTKGGEYKSKFVSGNIGKATF 116
 QY 181 RGLIVHSESGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIDL 227
 DB 117 KGLTFHLNBPSPFYDLFYTGQAESPLKIYEDNKTVESKFFHLDV 163

RESULT 53
 O54476 PRELIMINARY; PRT; 242 AA.
 ID O54476;
 AC O54476;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Staphylococcal enterotoxin K.
 GN Name=enk;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RM4282;
 RX MEDLINE=98385824; PubMed=9720870;
 RA Lindsay J.A., Ruzin A., Rose H.F., Kurepina N., Novick R.P.;
 RT "The gene for toxic shock toxin is carried by a family of mobile
 RT pathogenicity islands in Staphylococcus aureus.";
 RL Mol. Microbiol. 29:527-543(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RM4282;
 RA Barry P.C., Novick R.P.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U93688; AAC28968.1; -
 DR HSSP: P13380; 1KTX.
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR008992; Bact_endotox.
 DR InterPro: IPR006177; Bact_tox.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF01123; Staph_Strep_toxin; 1.
 DR Pfam: PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS: PR00279; BACTRLTOXIN_1
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 SQ SEQUENCE 242 AA; 27720 MW; 28CB4F2EE6B6B9 CRC64;

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Query Match      25.0%; Score 309; DB 2; Length 242;
Best Local Similarity 32.9%; Pred. No. 2.2e-17;
Matches 72; Conservative 40; Mismatches 81; Indels 26; Gaps 7;

QY 23 LSNLRQIYYNNEKATENKESDDQFLNTLLFKGFFTGHPWYNDLLVLDGSKDATTNKYG 82
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 29 IDNLRNFYTKDFFVDLKVNDPTPIANQLQF-----SNESY-DLISSEKDPNKFNFKG 82
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

QY 83 KKVLDYGAYYGQCGAGTPTNKACMYGGVTLHDNNRLTEKKVPINLWIDGKQTVPIDK 142
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 83 KKLDFVFGSYNGQC-----NTKYYIGGVTA-TNRYLDKSRNIPINIMINGNHKTISTNK 135
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

QY 143 VKTSKKEVTVQELDQARHYLHGKFGLY-----NSDSFGCK-----VQGLIYFHSSE 190
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 136 VSTNKKVYTAQEBIDVKLRKYLQEEYNYIYGHNGTKGGEYGHKSKFYSGFNIGKVTFLHNN 195
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

QY 191 GSTVSYDLF-DAQGYPPTLRIYDNKNTKINSENLHIDL 228
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 196 NDTFSYDLFYTGDGDLPKSPFLKIYEDNKTVESEKFLHDV 234
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

RESULT 54
QY 093CC5 PRELIMINARY; PRT; 242 AA.
AC 093CC5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Sek.
GN Name=sek;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COL;
RX MEDLINE=21935388; PubMed=11821418; DOI=10.1074/jbc.M111651200;
RA Yarwood J.M., McCormick J.R., Paustian M.L., Orwin P.M., Kapur V.,
RA Schlevert P.M.;
RT "Characterization and expression analysis of Staphylococcus aureus
RT pathogenicity island 3. Implications for the evolution of
RT staphylococcal pathogenicity islands."
RL J. Biol. Chem. 277.13138-13147(2002).
DR EMBL; AF410775; AAL04147.1; -.
DR HSSP; P13380; 1KTK.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bcstr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR Pfam; PF02876; Staph_Strep_tox_C_1.
DR PRINTS; PR00279; BACTR1TOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 242 AA; 27727 MW; 207938B99D9C9A9A CRC64;

Query Match      25.0%; Score 309; DB 2; Length 242;
Best Local Similarity 32.9%; Pred. No. 2.2e-17;
Matches 72; Conservative 40; Mismatches 81; Indels 26; Gaps 7;

QY 23 LSNLRQIYYNNEKATENKESDDQFLNTLLFKGFFTGHPWYNDLLVLDGSKDATTNKYG 82
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 29 IDNLRNFYTKDFFVDLKVNDPTPIANQLQF-----SNESY-DLISSEKDPNKFNFKG 82
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

QY 83 KKVLDYGAYYGQCGAGTPTNKACMYGGVTLHDNNRLTEKKVPINLWIDGKQTVPIDK 142
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 83 KKLDFVFGSYNGQC-----NTKYYIGGVTA-TNRYLDKSRNIPINIMINGNHKTISTNK 135
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

QY 143 VKTSKKEVTVQELDQARHYLHGKFGLY-----NSDSFGCK-----VQGLIYFHSSE 190
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 136 VSTNKKVYTAQEBIDVKLRKYLQEEYNYIYGHNGTKGGEYGHKSKFYSGFNIGKVTFLHNN 195
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

QY 191 GSTVSYDLF-DAQGYPPTLRIYDNKNTKINSENLHIDL 228
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 196 NDTFSYDLFYTGDGDLPKSPFLKIYEDNKTVESEKFLHDV 234
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

RESULT 54
QY 093CC5 PRELIMINARY; PRT; 242 AA.
AC 093CC5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Sek.
GN Name=sek;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COL;
RX MEDLINE=21935388; PubMed=11821418; DOI=10.1074/jbc.M111651200;
RA Yarwood J.M., McCormick J.R., Paustian M.L., Orwin P.M., Kapur V.,
RA Schlevert P.M.;
RT "Characterization and expression analysis of Staphylococcus aureus
RT pathogenicity island 3. Implications for the evolution of
RT staphylococcal pathogenicity islands."
RL J. Biol. Chem. 277.13138-13147(2002).
DR EMBL; AF410775; AAL04147.1; -.
DR HSSP; P13380; 1KTK.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bcstr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR Pfam; PF02876; Staph_Strep_tox_C_1.
DR PRINTS; PR00279; BACTR1TOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 242 AA; 27727 MW; 207938B99D9C9A9A CRC64;
```

```
QY 191 GSTVSYDLF-DAQGYPPTLRIYDNKNTKINSENLHIDL 228
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 196 NDTFSYDLFYTGDGDLPKSPFLKIYEDNKTVESEKFLHDV 234
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

RESULT 55
QY 096FM8 PRELIMINARY; PRT; 239 AA.
AC 096FM8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterococxin.
GN OrderedLocustNames=SAR1920;
OS Staphylococcus aureus (strain MRS252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=262458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnae.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Doud L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jørgels K.,
RA James K.D., Kennard N., Lane A., Mayes R., Moulie S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571856; CAG40906.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bcstr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR Pfam; PF02876; Staph_Strep_tox_C_1.
DR PRINTS; PR00279; BACTR1TOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR KW Complete proteome.
SQ SEQUENCE 239 AA; 27410 MW; 7AABC7A8AFC83FBB CRC64;

Query Match      24.4%; Score 302; DB 2; Length 239;
Best Local Similarity 33.0%; Pred. No. 8.1e-17;
Matches 72; Conservative 40; Mismatches 78; Indels 28; Gaps 7;

QY 25 NLKQIYYNNEKAIT--ENKESDDQFLNTLLFKGFFTGHPWYNDLLVLDGSKDATTNKYG 82
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 28 NLRN--YYGSIYPIEHQINPDNNRLSHQVFS-----KNSYTAFAFKVDEYKFKFN 79
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

QY 83 KKVLDYGAYYGQCGAGTPTNKACMYGGVTLHDNNRLTEKKVPINLWIDGKQTVPIDK 142
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 80 RAVDVYGSYGICYL-----NKKMYGGVTL-AGDYLEKSRICIPINLWVNGNLKTIISTDK 133
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

QY 143 VKTSKKEVTVQELDQARHYLHGKFGLYNSD-----SFGK-----VQGLIYFHSSE 190
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 134 VSTNKKVYTAQEBIDVKLRKYLQEEYNYIYGHNDTKGRNRYGTSKFFSGFNIGKVSFHLND 193
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

QY 191 GSTVSYDLFDAQGYPPTLRIYDNKNTKINSENLHIDL 228
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 194 GTSFSYDLFDGTGQABESFLKIYDNKKTVEIDKFLHDV 231
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

RESULT 56
QY ETVX STAAU STANDARD; PRT; 266 AA.
AC P01552;
DT 21-JUL-1986 (rel. 01, Created)
```

DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DE 25-OCT-2004 (Rel. 45, Last annotation update)
 DT Enterotoxin type B precursor (SEB).
 GN Name=entB;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86168029; PubMed=3957869;
 RA Jones C.L., Khan S.A.;
 RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus."
 RL J. Bacteriol. 166:29-33(1986).
 RP SEQUENCE OF 40-91 FROM N.A.
 RX MEDLINE=85298255; PubMed=3898073;
 RA Rameilii D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;
 RT "Molecular cloning of staphylococcal enterotoxin B gene in Escherichia coli and Staphylococcus aureus."
 RL Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).
 RP [3]
 RX SEQUENCE OF 28-266 (S-6).
 RA MEDLINE=71007902; PubMed=5470821;
 RL Huang I.-Y., Bergdoll M.S.;
 RT "The primary structure of staphylococcal enterotoxin B. 3. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence."
 RL J. Biol. Chem. 245:3518-3525(1970).
 RP [4]
 RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RA MEDLINE=93063291; PubMed=1436058; DOI=10.1038/359801a0;
 RL Swaminathan S., Purey W.F. Jr., Pletcher J., Sax M.;
 RT "Crystal structure of staphylococcal enterotoxin B, a superantigen."
 RL Nature 359:801-806(1992).
 RP [5]
 RX X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
 RA MEDLINE=94203282; PubMed=8152483; DOI=10.1038/368711a0;
 RL Jardenzky T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G., Chi Y.T., Stauffer C., Strominger J.L., Wiley D.C.;
 RT "Three-dimensional structure of a human class II histocompatibility molecule complexed with superantigen."
 RL Nature 368:711-718(1994).
 RP [6]
 RX X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.
 RA MEDLINE=99096298; PubMed=9881971; DOI=10.1016/S1074-7613(00)80646-9;
 RL Li H., Llera A., Tsuchiya D., Leder L., Yseern X., Schlievert P.M., Karjalainen K., Mariuzza R.A.;
 RT "Three-dimensional structure of the complex between a T cell receptor beta chain and the superantigen staphylococcal enterotoxin B."
 RL Immunity 9:807-816(1998).
 RP [7]
 RX X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RA MEDLINE=98181012; PubMed=9514739; DOI=10.1006/jmbi.1997.1577;
 RL Papageorgiou A.C., Tranter H.S., Acharya K.R.;
 RT "Crystal structure of microbial superantigen staphylococcal enterotoxin B at 1.5-A resolution: implications for superantigen recognition by MHC class II molecules and T-cell receptors."
 RL J. Mol. Biol. 277:61-79(1998).
 RP -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>)

CC or send an email to license@sib.ch.
 CC EMBL: M1118; AAA8550.1; -.
 DR PIR: S27360; ENSAB6.
 DR PDB: 1D5M; X-ray; C=28-266.
 DR PDB: 1D5X; X-ray; C=28-266.
 DR PDB: 1D5Z; X-ray; C=28-266.
 DR PDB: 1D6E; X-ray; C=28-266.
 DR PDB: 1SBB; X-ray; B/D=28-266.
 DR PDB: 1SR3; X-ray; @=28-266.
 DR PDB: 1SR4; X-ray; @=28-266.
 DR PDB: 1SEB; X-ray; D/H=29-262.
 DR PDB: 2SEB; X-ray; D=28-266.
 DR PDB: 3SEB; X-ray; @=28-265.
 DR InterPro: IPR008992; Bact_endotox.
 DR InterPro: IPR006123; Bact_tox.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006126; Staph/Strep_tox.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF02876; Staph_Strep_tox_C; 1.
 DR Pfam: PF01123; Staph_Strep_toxin; 1.
 DR PRINTS: PR00279; BACTRTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW 3D-structure; Direct protein sequencing; Enterotoxin; Signal;
 KW Superantigen; Toxin.
 FT SIGNAL 1 27
 FT CHAIN 28 266
 FT DISULFID 120 140
 FT CONFLICT 56 58
 FT CONFLICT 69 77
 FT CONFLICT 118 118
 FT CONFLICT 128 130
 FT CONFLICT 133 135
 FT CONFLICT 149 150
 FT CONFLICT 156 156
 FT CONFLICT 185 186
 FT CONFLICT 233 233
 FT CONFLICT 246 247
 FT STRAND 29 29
 FT HELIX 41 43
 FT STRAND 44 44
 FT TURN 48 48
 FT HELIX 49 52
 FT HELIX 53 55
 FT STRAND 60 66
 FT STRAND 69 69
 FT TURN 73 74
 FT STRAND 75 78
 FT TURN 83 85
 FT STRAND 90 94
 FT HELIX 98 104
 FT TURN 105 106
 FT STRAND 108 113
 FT STRAND 116 116
 FT TURN 118 119
 FT TURN 127 128
 FT STRAND 138 142
 FT STRAND 145 147
 FT TURN 149 150
 FT STRAND 152 155
 FT TURN 166 167
 FT STRAND 168 179
 FT STRAND 181 183
 FT HELIX 184 199
 FT STRAND 209 218
 FT TURN 219 220
 FT STRAND 221 226
 FT STRAND 232 232
 FT HELIX 237 241
 FT STRAND 242 246
 FT TURN 249 251
 FT TURN 252 254

DDN -> NND (in Ref. 3).
 DQFLYFDLI -> NEFFDLYL (in Ref. 3).
 Missing (in Ref. 3).
 DIN -> NND (in Ref. 3).
 QTD -> ENT (in Ref. 3).
 NG -> GN (in Ref. 3).
 Y -> YF (in Ref. 3).
 OE -> EQ (in Ref. 3).
 D -> N (in Ref. 3).
 DN -> ND (in Ref. 3).

FT	STRAND	255	263
SQ	SEQUENCE	266 AA; 31436 MW;	B6D417F61CF018B0 CRC64;
Query Match		24.3%;	Score 300.5; DB 1; Length 266;
Best Local Similarity		33.6%;	Pred. No. 1.2e-16;
Matches	82; Conservative	47;	Mismatches 96; Indels 19; Gaps 8
QY	1	SEKSEINEKDLRKKSELQRNALISLRLQIYYVNEKAITENKESDDQFLENTILLFKGFFTG	60
Db	27	AESQDPKPDELHNSKF-TGLMEMMKYLVDNNHSAL-NVKSIDQFLVFEDLLYSIKDKTK	84
QY	61	HPWINDLIVDJSGSKATNRYKSKVDLYAYYYGYC-----AGSTPNKTACMYGG	110
Db	85	LGNVDNVVEEFNKDLADKYDKDYDFVSANYYYOCYFESEKTNIDINSHQTDRAKTKTMYGG	144
QY	111	VTLGDHNRLTEEEKVPINLMIDGKOTVAIDPKTSSKEEVVOELDLQAHYLHGKFGFY	170
Db	145	VTEHNGNDLDKTRISTAVRVEDGK-NLSFD-VQINKKRVTAQOELDYLIRHYLVKRKKLY	202
QY	171	NDSDFGKVQRGLIVFHSSSEGSTVSYDLFDQAQQYPD--TLRLRYDNKTTINSNLHLID	228
Db	203	EFPNN--SPYEYGVIKFIENENS-FWYDMMPAPGCDKFSKYLMMYDNNKWDVSDKVIEY	259
QY	229	YLXT 232	
Db	260	YLTT 263	

RESULT	57
06YCN4	PRELIMINARY; PRT; 261 AA.
ID	06YCN4
AC	05-JUL-2004 (TREMBLrel. 27, Created)
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE	Enterotoxin SEU variant.
OS	Staphylococcus aureus.
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX	NCPI_taxid=1280;
FN	(1)
RP	SEQUENCE FROM N.A.
RC	STRAIN=382F;
RX	MEDLINE=22692404; PubMed=12807452;
RA	Lefevre C., Perelle S., Dlasser F., Fach P.;
RT	"Identification of a new putative enterotoxin SEU encoded by the egc
RL	cluster of Staphylococcus aureus."
RT	J. Appl. Microbiol. 95:38-43 (2003).
EMBL	AY158703; AA017732.1; -
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0009405; P:pathogenesis; IEA.
DR	InterPro; IPR008992; Bact_endotox.
DR	InterPro; IPR006123; Staph/Strep_toxin.
DR	InterPro; IPR006126; Staph/Strep_tox.
DR	InterPro; IPR006173; Staph_tox_OB.
DR	Pfam; PF01123; Staph_strep_toxin; 1.
DR	Pfam; PF02876; Staph_strep_tox_C; 1.
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_2; 1.
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SO	SEQUENCE 261 AA; 30547 MW; A407E960CC5974B0 CRC64;
Query Match	24.1%; Score 298; DB 2; Length 261;
Best Local Similarity	31.5%; Pred. No. 1,9e-16;
Matches	80; Conservative 49; Mismatches 79; Indels 46; Gaps 13
Oy	3 KSEETNECDLRKSKSEIQRNALNLRQIYYNEKALTE-NKESDQPLENTLFFKGFPTGH 61
Db	25 KPEQDN-----KASEP-TGLMDNMR--YLYDDGVSEINIKAEKFLQHDLLFK----- 70
Oy	62 PWYNLDLVLDLGSK-----DATNKKYKGGKVDLYGAYGYGACAGTNP-----K 103
Db	71 --INGSKD-GSKILKTEFRNNNSLSKTYKNKQIDLFCTNYIYQCYSSADNMEINDGRLE 127
Oy	104 TACMTGGVATLHDNNRLTBEKKV--PINLMI---DGKQTTPVLDKVTSSKKEVTVQELDQ 158

Db	128	KTCMYGGVTEHGDGNQLDKNNSTDNHNLITIKYFENIERSS-LFD-I	PNNKNIITAQOEIDYK	186
Qy	159	ARRYLHGRGGLKNSDFGKQGRGLIVHSSGSTVSYLEDAQO--Y	PDTLIRIRYDN	216
Db	187	VRRYLHLKHLKLEFNS--SPYETGYIKFIEGNGHSFWYDMMPESGEK	YFPTKILLIYNDN	244
Qy	217	KTINSENHLIDLYL	230	
Db	245	KTIVESKINVEVHL	258	

RESULT 58	06GFNO	PRELIMINARY;	PRT;	261 AA.
AC	06GFNO;			
AD	05-JUL-2004 (TrEMBLrel. 27, Created)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)			
DE	Enterotoxin.			
CN	OrderedLoccusNames=SB1918;			
OS	Staphylococcus aureus (strain MRSA252).			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=282458;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
EX	PubMed=15213324; DOI=10.1073/pnas.0402521101;			
RA	Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,			
RA	Enright M.C., Foster T.J., Moore C.E., Huret L., Atkin R., Barron A.,			
RA	Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,			
RA	Churcher C., Clark L., Cotton C., Cronin A., Duggett J., Dowd L.,			
RA	Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jasele K.,			
RA	James K.D., Lennard N., Little A., Mayes R., Moule S., Mungall K.,			
RA	Armond D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,			
RA	Sharp S., Simmonds M., Stevens K., Whitehead S., Barrrell B.G.,			
RT	Spratt B.G., Parkhill J.;			
RT	"Complete genomes of two clinical Staphylococcus aureus strains:			
RL	Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004)."			
DR	EMBL; BX571856; CAG40904.1; .			
DR	GO; GO:0005576; C:extracellular; IEA.			
DR	GO; GO:0009405; P:pathogenesis; IEA.			
DR	InterPro; IPRO08992; Bact_endotox.			
DR	InterPro; IPRO06123; Staph/Strep toxin.			
DR	InterPro; IPRO06126; Staph/Strep toxin.			
DR	InterPro; IPRO06173; Staph_tox_08.			
DR	Pfam; PF01123; Staph_Scrp_toxin; 1.			
DR	Pfam; PF02876; Staph_Scrp_tox_C; 1.			
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.			
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.			
KW	Complete proteome.			
SO	SEQUENCE 261 AA; 30547 MW; A407B960CC5974B0 CRC64;			
Query Match	24.1%; Score 298; DB 2; Length 261;			
Best Local Similarity	31.5%; Pred. No. 1.9e-16;			
Matches 80; Conservative 49; Mismatches 79; Indels 46; Gaps 133				
QY	3 KSEINTEKRLKKSSELRGALSNLFOIYYNEKATTE-NKESDQPLENTLLFEGFPTGH 61			
DB	25 KPEQLN-----KASEP-TGLMDNMR--LYLDDKHSEINIAQEPFLQHDLLFK----- 70			
QY	62 PWNNDLLVDLGSK-----DATNKKKGKGVLDYGYVYGQAGAGTPN-----K 103			
DB	71 --INGSKID-GSKILKTEFPNNNSLSDKTKKKNIDLFGNYYIYQCYFSDNDELNDGRLE 122			
QY	104 TACMYGVTLLHNNRLTEERKV--DINIMI--DGKQTVPIDKVTYSKKEVTVQELDLQ 156			
DB	128 KTCMYGVTIEHDQNDQDKNNSSTDNSHNILIKVFERNRSLSPD-IPTNKKNIITQAEIDYK 166			
QY	159 ARRYHLGKGLVNSDFGKQVQRGLIVHSSRGVSVDLDDAGQ--YPTTLRIYRDN 216			
DB	187 VRRYLLKHKLVLEFNS--SPYETGYIKTEGNGHSFWDDMPESGSKRYPTFKYLLIYND 244			

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QY      217 KTINSENLHIDL 230
DB      245 KTVESKINVEVHL 258

RESULT 59
SPEA STRP8 STANDARD; PRT; 251 AA.
AC P62561; P08095;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
DE (SPE A).
GN Name=spea; OrderedLocusNames=spym18_0393;
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxId=186103;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232 / Serotype M18;
RX PubMed=11917108; DOI=10.1073/pnas.062526099;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veary L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks."
RT Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
CC -!- FUNCTION: Causative agent of the symptoms associated with scarlet
CC fever, have been associated with streptococcal toxic shock-like
CC disease and may play a role in the early events of rheumatic fever
CC (By similarity).
CC -!- SUBUNIT: Binds to major histocompatibility complex class II beta
CC chain (By similarity).
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
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CC -----
EMBL: AE009982; ALU97141.1; -.
DR InterPro: IPR0088992; Bact_endotox.
DR InterPro: IPR006177; Bact_Tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph/Strep_OB.
DR Pfam: PF02876; Staph-Strep_tox_C1.
DR Pfam: PF01123; Staph-Strep_toxin; 1.
DR PRINTS: PRO0279; BACTRITOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome; Signal; Toxin.
FW SIGNAL 1 30 By similarity.
FT CHAIN 31 251 Exotoxin type A.
FT DISULFID 117 128 By similarity.
SQ SEQUENCE 251 AA; 29246 MW; 54001FE4CCBFC3 CRC64;

Query Match 23.9%; Score 295.5; DB 1; Length 251;
Best local similarity 34.2%; Pred. No. 2,9e-16;
Matches 81; Conservative 45; Mismatches 92; Indels 19; Gaps 10;

QY 4 SEEINKEKDKKSELOKRNAL-SNLRQIYV-YNEKAIT-ENKESDDQFLNLTLLFKGFTTG 60
DB 25 SQEVFAQODPDDPQLHSSSLVKNLQNIYFPEGDPVTHENVKSVQDLTSHDLIYN--VS 81

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QY      61 HPMYNDLVLDGSKATNKYKGVLDYGAYYGYOC-AGCTNKTACWYGVTLHDNNRL 119
DB      82 GPNYDKLKTLEKLNQEMATLFKDNVDIYGEVEYHLCYLCENERSACTIGVTHNEGNHL 141
QY      120 TEKKVPIINLWIDGQTVPIIDKVTSKKEVTVQELDQARHYLKGKFGLYNSDSFGKRV 179
DB      142 EIPKRIIVKVSIDGLO-SLSFD-IETNKKMTVAQELDIYKRVKXLDNKKLYNNGP--SKY 197
QY      180 QRGILVFHSSEGSITVSYDLFD---AGQYPTLLRIYRDNKTINSENLHIDL 232
DB      198 EGVYIKFPIKNNKSEFWPDEFPEPEFTQSKY----LMYVDNETLDSNTSQIRVYLT 250

RESULT 60
SPEA STRPY STANDARD; PRT; 251 AA.
AC P62560; P08095;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
DE (SPE A).
GN Name=spea;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxId=1314;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86166804; PubMed=3514452;
RA Weeks C.R., Ferretti J.D.;
RT "Nucleotide sequence of the type A streptococcal exotoxin
RT (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
RT T12."
RL Infect. Immun. 52:144-150(1986).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=86284313; PubMed=3526093;
RA Johnson L.P., U'Italian J.U., Schlievert P.M.;
RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
RT related to Staphylococcus aureus enterotoxin B."
RL Mol. Gen. Genet. 203:354-356(1986).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).
RX MEDLINE=99094887; PubMed=9878045; DOI=10.1093/emboj/18.1.9;
RA Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,
RA O'Brien S.M., Tranter H.S., Acharya K.R.;
RT "Structural basis for the recognition of superantigen streptococcal
RT pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell
RT receptors."
RL EMBO J. 18:9-21(1999).
CC -!- FUNCTION: Causative agent of the symptoms associated with scarlet
CC fever, have been associated with streptococcal toxic shock-like
CC disease and may play a role in the early events of rheumatic
CC fever.
CC -!- SUBUNIT: Binds to major histocompatibility complex class II beta
CC chain.
CC -!- MISCELLANEOUS: This toxin seems to be coded by bacteriophage T12.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
EMBL: U40453; AAC48868.1; -.
DR EMBL: X03929; CA27568.1; -.
DR PIR: A26152; A26152.
DR PDB: 1B12; X-ray; -.

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DR PDB; 1FNU; X-ray; --
DR PDB; 1FNU; X-ray; --
DR PDB; 1FNU; X-ray; --
DR PDB; 1H45; X-ray; --
DR PDB; 1LOX; X-ray; --
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_Strep_tox_C1.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR PRINTS; PR00279; BACTR1TOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW 3D-structure; Signal; Toxin.
FT SIGNAL 1 30
FT CHAIN 31 251
FT DISULFID 117 128
FT CONFLICT 6 6
FT CONFLICT 17 18
FT CONFLICT 25 35
FT CONFLICT 40 40
FT CONFLICT 43 43
FT CONFLICT 47 59
FT CONFLICT 129 129
FT CONFLICT 165 178
FT TURN 36 38
FT HELIX 42 44
FT TURN 46 48
FT HELIX 49 56
FT STRAND 60 65
FT STRAND 69 74
FT TURN 73 78
FT STRAND 75 78
FT STRAND 82 82
FT TURN 83 84
FT STRAND 85 85
FT STRAND 87 91
FT HELIX 95 102
FT TURN 103 103
FT STRAND 106 110
FT TURN 113 113
FT TURN 115 116
FT TURN 121 122
FT STRAND 126 130
FT STRAND 133 135
FT TURN 137 138
FT STRAND 140 153
FT TURN 154 155
FT STRAND 156 167
FT STRAND 169 171
FT HELIX 172 186
FT STRAND 197 205
FT STRAND 212 215
FT HELIX 224 227
FT HELIX 228 231
FT TURN 232 233
FT STRAND 236 238
FT TURN 239 241
FT STRAND 243 251
SQ SEQUENCE 251 AA; 29246 MW; 54001FB4CCBCFC3 CRC64;

Query Match 23.9%; Score 295.5; DB 1; Length 251;
Best Local Similarity 34.2%; Pred. No. 2.9e-16;
Matches 81; Conservative 45; Mismatches 92; Indels 19; Gaps 10;

4 SBEINERKLRKSELRNAL-SNLRQIYY-VNEKAIT-ENKSDQOFLENTLLFKGFFLG 60
DB 25 SOEVFAOODPPPSQLHRSSLVNQLNLIYFLVGBDVHTENKVSVDQLSLHLIYN--VS 81
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QY 61 HPWYNDDLVDIGSDATITKKGKVDLYGAYYQC-AGTTPNKTACMYGVTILHDNRL 119
DB 82 GPNYDKLTTELKNOEMATLFDXKNVDIYGVYHLCYLCEAENRSACIYGVVTHNEGHL 141
QY 120 TEEKVPINLWIDGKQOTVPIDKVTSKEVTVOELDQARHYLHGKFGLYNSDFGSKV 179
DB 142 EIPKIVKVSIDGIQ-SLSPD-IEINKMVTAOELDYKAKRYLTDNKQLYTNGP--SKY 197
QY 180 QRLIVFHSSEGSTVSYDLFD---AQOQYPTLLRIYRDNKTINSEMHIDLILYT 232
DB 198 ETGYIKKFIIPKNKESWPFPEPEPTQSKY----LMYKONETLSDNTSQLEVLILT 250

RESULT 61
Q6RIY7 PRELIMINARY; PRT; 177 AA.
ID Q6RIY7;
AC Q6RIY7;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Enterotoxin type M variant (Fragment).
OS Staphylococcus aureus subsp. aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=46170;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19095;
RX PubMed=1513181;
RA Sergeev N., Volokhov D., Chiznikov V., Rasooly A.;
RT "Simultaneous analysis of multiple staphylococcal enterotoxin genes by
RT an oligonucleotide microarray assay.";
RL J. Clin. Microbiol. 42:2134-2143(2004).
DR EMBL; AY518772; AAR99712.1; -.
DR HSSP; P13380; 1AN8.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR Pfam; PF02876; Staph_Strep_tox_C1.
DR PRINTS; PR00279; BACTR1TOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1 177
FT NON_TER 1 177
SQ SEQUENCE 177 AA; 20215 MW; C6CCD70E5D7B3443 CRC64;

Query Match 23.8%; Score 295; DB 2; Length 177;
Best Local Similarity 37.7%; Pred. No. 2.1e-16;
Matches 61; Conservative 31; Mismatches 52; Indels 18; Gaps 4;

79 KYGKKVDLYGAYYQCAAGTTPNKTACMYGVTILHDNRLTEEKVPINLWIDGKQTV 138
DB 22 KFKNRAVDVYGLSYSGYL-----KNKMYGVTIL-AGDYLEKRCRCPINLWVNGNHTI 75
QY 139 PIDKVTSKKEVTVOELDQARHYLHGKFGLYNSD-----SFGK-----VORGLIVF 186
DB 76 STDKYSTKKIIVTAQELDTKARLYQSEYINITYGRNDTKKGNKGYGKSKFSGFNTKISF 135
QY 187 HSEGSTVSYDLFDPAQOQYPTLLRIYRDNKTINSEMHIDL 228
DB 136 HUNDGTSFSDLPDTGTQGAESFLKIYVDNKTIVETDKFLDV 177

RESULT 62
Q6K6K5 PRELIMINARY; PRT; 251 AA.
ID Q6K6K5;
AC Q6K6K5; 079XZ6;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Enterotoxin type A-phage associated (SpeA precursor).
```

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GN Name=spea3; OrderedLocName=SPe0560, SPYM3_1301;
OS Streptococcus pyogenes (serotype M3);
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus;
OX NCBI_TaxID=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
RA Bares S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
emergence.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1;
RX MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
Hayashi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
large-scale genomic rearrangement in invasive strains and new insights
into phage evolution.";
RT Genome Res. 13:1042-1055(2003).
DR EMBL; AB014161; AM79908.1; -.
DR EMBL; AP005142; BAC63655.1; -.
DR PIR; A60108; A60108.
DR HSSP; P01552; 1SER.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
SQ SEQUENCE 251 AA; 29260 MW; 05E782CDA01BFCD5 CRC64;

Query Match 23.8%; Score 294.5; DB 2; Length 251;
Best Local Similarity 33.8%; Pred. No. 3.6e-16;
Matches 80; Conservative 46; Mismatches 92; Indels 19; Gaps 10;

QY 4 SEINEKDKRKSELRNAL-SNLRQIYY-YNEKAIT-ENKESDDPLENTLLFKGPFPG 60
DB 25 SQEIVFAQOPDPSQLRRSSLVKVLQNIYLFEGDPYTHENVKSVDDLLSHDLIN--VS 81
QY 61 HFWYNDLVLDGSKATNKYKGVLDYGAHYGQC-AGSTPKTKTCMTGVTLHDNNRL 119
DB 82 GPNYDGLKTELKNOEWALFKDKNIDYGVYHLCYLCENARSAICYIGVYTNHGNNL 141
QY 120 TEKKKVPINLMDIGKQTVPIPVKVTSKKEVTVQELDLQARHVLHGFGLYNSDSFGKY 179
DB 142 ELPKXIVVAVYIDGIG-SLSPD-IETNKKAVTAQELDYKRAKYLTDNKKLYTNGP--SKY 197
QY 180 QRGILVFHSSEGSVSYDLFD---AQGYPTLRLIRYDNKTINSENLHIDLVLVT 232
DB 198 EGVYIKFIPKNKSEFMFDFPEPEFQSKX---LMIYKDNELTDSNTSQTIVYLT 250

RESULT 63
Q6XXM3 PRELIMINARY; PRT; 261 AA.
AC Q6XXM3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
```

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DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Enterotoxin Seu.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=383F;
RX MEDLINE=22692404; PubMed=12807452;
RA Leterre C., Perelle S., Dillasser F., Fach P.;
RT "Identification of a new putative enterotoxin seu encoded by the egc
cluster of Staphylococcus aureus.";
RT J. Appl. Microbiol. 95:38-43(2003).
DR EMBL; AY205307; AAP41903.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 261 AA; 30535 MW; 663E32AF13794877 CRC64;

Query Match 23.5%; Score 291.5; DB 2; Length 261;
Best Local Similarity 31.0%; Pred. No. 6.6e-16;
Matches 74; Conservative 50; Mismatches 90; Indels 25; Gaps 9;

QY 10 KDLRKSELRNALSNLRQIYYNEKAIT-EKESDDPLENTLLFKGPFPGHWNLDL 68
DB 27 EQLNKASEFS-GLMDNR--YVDDKAVSETIKQAQKQLQDLDFKNGSKIDSKILK 83
QY 69 VDLGSKATNKYKGVLDYGAHYGYCAGTGN-----KTACMYGVTLHDNNRL 119
DB 84 TEFNKKSLSDKXKKNKVDLFGTNYNQCYFSADNNEMLNDGRLLIEKTCMYGVTEDHGNOI 143
QY 120 TEKK-----KVPINLMDIGKQTVPIPVKVTSKKEVTVQELDLQARHVLHGFGLYNSD 173
DB 144 DKNNLTDNSHNLIKYV-ENERTLSFD-ISTNMKNITQOEIDYKRVNLLKRNKLYERN 201
QY 174 SFGKQGRGLIVFHSSEGSVSYDLFDAQGO--YPTTLRLIRYDNKTINSENLHIDLVL 230
DB 202 S--SPYSGYIKFIEGNSHFWYDMMPSEGEKFPYTKYLLINDKTVASKSINVEVHL 258

RESULT 64
Q6XXM5 PRELIMINARY; PRT; 261 AA.
AC Q6XXM5;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Enterotoxin Seu.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=352B;
RX MEDLINE=22692404; PubMed=12807452;
RA Leterre C., Perelle S., Dillasser F., Fach P.;
RT "Identification of a new putative enterotoxin seu encoded by the egc
cluster of Staphylococcus aureus.";
RT J. Appl. Microbiol. 95:38-43(2003).
DR EMBL; AY205305; AAP41901.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006123; Staph/Strep_toxin.
```


RC STRAIN-AS14;
RA Blaiotta G., Pennacchia C., Casaburi A., Ercolini D., Fusco V.,
RL Villani F.,
DR Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY291445; AAP78526.1; -.
DR HSSP; P13163; IESF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:patogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_toxin.
DR Pfam; PF01123; Staph_stp_toxin; 1.
DR Pfam; PF02876; Staph_stp_toxin; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER
FT SEQUENCE 218 AA; 24993 MW; 6988B8CE49754350 CRC64;

Query Match 23.2%; Score 287.5; DB 2; Length 218;
Best Local Similarity 34.0%; Pred. No. 1.1e-15;
Matches 70; Conservative 34; Mismatches 69; Indels 33; Gaps 7;

QY 23 LSNLRQIY----YNEKAITENKESDDQPLENTLLFKGFFTHPMYNDLLVLDGSKDATN 78
DB 30 VGNLRFYTKHDYIDLKGVTDKPLPIANQLE-----FSTG---TNDLISSNWDEIS 79
QY 79 KKGKKVDLYGAYVYQACAGTPNKTACMYGVTLDHNNRLTEKKVPIINLWIDGKQTV 138
DB 80 KKGKKLDIFGIDYNGPC-----KSKYWGATL--SGOYLNSARKIPINLWNGKHKTI 132
QY 139 PIDKVTSKKEVTVQELDLQARHYLHGKFLYNSDSFG-GK-----VQGLIVF 186
DB 133 STDKATNKGLVTAQIDVKTARLYQEEVNIYGHNTGKGYKSKFYSGFNNKVL 192
QY 187 HSESGTWSYDLFPAQGYPTLLRI 212
DB 193 HLNNEKSFSDYDLFTGDLVPSFLKI 218

RESULT 68
Q7X0E9 PRELIMINARY; PRT; 218 AA.
AC Q7X0E9;
DT 01-OCT-2003 (TEMBLrel. 25, Last Created)
DT 01-OCT-2004 (TEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Enterotoxin type I (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI;
RA Blaiotta G., Pennacchia C., Casaburi A., Ercolini D., Fusco V.,
RL Villani F.,
DR Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY291443; AAP78522.1; -.
DR HSSP; P13163; IESF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:patogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_toxin.
DR Pfam; PF01123; Staph_stp_toxin; 1.
DR Pfam; PF02876; Staph_stp_toxin; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER
FT SEQUENCE 218 AA; 24994 MW; 698329CE49754350 CRC64;

Query Match 23.1%; Score 286.5; DB 2; Length 218;
Best Local Similarity 34.0%; Pred. No. 1.4e-15;
Matches 70; Conservative 34; Mismatches 69; Indels 33; Gaps 7;

QY 23 LSNLRQIY----YNEKAITENKESDDQPLENTLLFKGFFTHPMYNDLLVLDGSKDATN 78

DB 30 VGNLRFYTKHDYIDLKGVTDKPLPIANQLE-----FSTG---TNDLISSNWDEIS 79
QY 79 KKGKKVDLYGAYVYQACAGTPNKTACMYGVTLDHNNRLTEKKVPIINLWIDGKQTV 138
DB 80 KKGKKLDIFGIDYNGPC-----KSKYWGATL--SGOYLNSARKIPINLWNGKHKTI 132
QY 139 PIDKVTSKKEVTVQELDLQARHYLHGKFLYNSDSFG-GK-----VQGLIVF 186
DB 133 STDKATNKGLVTAQIDVKTARLYQEEVNIYGHNTGKGYKSKFYSGFNNKVL 192
QY 187 HSESGTWSYDLFPAQGYPTLLRI 212
DB 193 HLNNEKSFSDYDLFTGDLVPSFLKI 218

RESULT 69
Q06531 PRELIMINARY; PRT; 239 AA.
AC Q06531;
DT 01-NOV-1996 (TEMBLrel. 01, Last Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; PubMed=8406814;
RA Marx J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications";
RL Infect. Immun. 61:4254-4262 (1993).
DR EMBL; L13374; AAA26518.1; -.
DR HSSP; P23313; 1KLD.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:patogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006173; Bactl_toxin.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_toxin.
DR Pfam; PF01123; Staph_stp_toxin; 1.
DR Pfam; PF02876; Staph_stp_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER
FT SEQUENCE 239 AA; 27612 MW; BB7BD6204731ED24 CRC64;

Query Match 23.1%; Score 285.5; DB 2; Length 239;
Best Local Similarity 32.1%; Pred. No. 1.8e-15;
Matches 75; Conservative 49; Mismatches 91; Indels 19; Gaps 9;

QY 11 DLAKSELQNALSNLRQIYYNEKAITENK-BSDDQPLENTLLFKGFFTHPMYNDLLV 69
DB 10 DLKSSSP-TGTGNMNM--LYLDHYVSATKVSVDKFLAHDLIYINSDRLKMYDVKT 66
QY 70 DLGSKDATNKYKKGKVDLYGAYVYQAC-----AGTPNKTACMYGVTLDHNNRLTEE 122
DB 67 ELINDELAKKYKQVDVYGSNNYVNCYFSSKDNVKGVTGKTCMYGGITKHEGNHNDG 126
QY 123 --KKVPIINLWIDGKQTVPIDKVTSKKEVTVQELDLQARHYLHGKFLYNSDSFGKQV 180
DB 127 NLQNVLVAVRY-ENKRYTISFE-VQTDKSVTAQELIKANFLINKNLYEENS--SPYE 182
QY 181 RGLIVFHSSGTSYSDLPFAQGYPT--TLRIYRDNKTINSENLHIDLIVLT 232
DB 183 TGYIKFLNNGNFTWDMFAPDQKFDQSKYILMNTKNTVDSKSKYKIVHLTT 236

RESULT 70

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Q06532      PRELIMINARY;      PRT;      239 AA.
AC Q06532;
DT 01-NOV-1996 (TREMblrel. 01. Created)
DT 01-NOV-1996 (TREMblrel. 01. Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25. Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; PubMed=8406814;
RA Marx J.C., Lyon J.D., Roberson J.R., Lupter M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262 (1993).
DR EMBL; I13375; AAA26619.1; -.
DR HSBP; P23313; IKLU.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactr_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin_1.
DR Pfam; PF02876; Staph_strep_tox_C_1.
DR PRINTS; PR00279; BACTRTOXIN_
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27642 MW; C77009F46BC8D645 CRC64;

Query Match 23.1%; Score 285.5; DB 2; Length 239;
Best Local Similarity 32.1%; Pred.No.18e-15;
Matches 75; Conservative 49; Mismatches 91; Indels 19; Gaps 9;

QY 11 DLRRKSELQRNALSNLRQIYYNEAITEKN-ESDDQFLENTLPKGFPTGHPWYNDLLV 69
Db 10 DLHSSSE-TGTMDMK--VLYDDHYVATKYKSDVKFLADLIYNISDKLKNADKYKT 66
QY 70 DLGSKDATNKKYKKKVDLYGAYYGYQC-----AGTPNKTCMYGVTLLHNNRLTEE 122
Db 67 ELLNEDLAKKYYDEVDVGYGNYNVCYFSSKDNVGYGKTCMYGGITKEGHPNDG 126
QY 123 --KKVPILMLDGGKQTTVPIDKVTSKKEVYQGEIDLAQAHYLAHKKFGJYNSDSFGKQV 180
Db 127 NLQNVLAIVY-BNKKNTISFE-VQTDKKSVTAGQBLDIFARNFLINKKQVLEFNS--SPYE 182
QY 181 RGLIVFHSSEGSVSYDLPDAQGYPD--TLIRIYRDNKNTINSENMLIDLYLT 232
Db 183 TGYIKFIENNNTFWYDMMPARGDKFDQSKYLMWYNDKTKVDSKVKLEVHLTT 236

RESULT 71
ETC3 STAM STANDARD; PRT; 266 AA.
AC P23313;
DT 01-NOV-1991 (Rel. 20. Created)
DT 01-NOV-1991 (Rel. 20. Last sequence update)
DT 25-OCT-2004 (Rel. 45. Last annotation update)
DE Enterotoxin type C-3 precursor (SEC3).
GN Name=etc3; OrderedLocNames=SAV2009, SA1817;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879, 158879, 1280;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Mu50 / ATCC 700699, and N315;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;

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RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratsuki K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90220508; PubMed=2325627;
RA Hovde C.U., Hackett S.P., Bohach G.A.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
RT sequence comparison of all three type C staphylococcal enterotoxins.";
RL Mol. Gen. Genet. 220:329-333 (1990).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH TCR.
RX MEDLINE=97064178; PubMed=8906797; DOI=10.1038/384188a0;
RA Fields B.A., Malchiodi E.L., Li H., Ysern X., Stauffacher C.V.,
RA Schlievert P.M., Karjalainen K., Mariuzza R.A.;
RT "Crystal structure of a T-cell receptor beta-chain complexed with a
RT superantigen.";
RL Nature 384:188-192 (1996).
CC -1 FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -1 SUBCELLULAR LOCATION: Secreted.
CC -1 SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; AP003364; BAB58171.1; -.
CC EMBL; AP003135; BAB43097.1; -.
CC EMBL; X51661; CAA35972.1; -.
CC PIR; S11885; S11885.
CC PDB; 1JCK; X-ray; B/D=28-266.
CC PDB; 1JMM; X-ray; D=28-266.
CC PDB; 1JMS; X-ray; D=28-266.
CC PDB; 1JWU; X-ray; D=28-266.
CC PDB; 1KLU; X-ray; D=28-266.
CC InterPro; IPR008992; Bact_endotox.
CC InterPro; IPR006177; Bactr_tox.
CC InterPro; IPR006123; Staph/Strep_toxin.
CC InterPro; IPR006126; Staph/Strep_tox.
CC InterPro; IPR006173; Staph_tox_OB.
CC Pfam; PF02876; Staph_strep_tox_C_1.
CC Pfam; PF01123; Staph_strep_toxin_1.
CC PRINTS; PR00279; BACTRTOXIN.
CC PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
CC PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW 3D-structure; Complete proteome; Enterotoxin; Signal; Superantigen;
KW Toxin.
FT SIGNAL 1 27
FT CHAIN 28 266 Enterotoxin type C-3.
FT DISULFID 120 137
FT HELIX 35 37
FT HELIX 41 43
FT STRAND 44 44
FT STRAND 48 48
FT HELIX 49 55
FT STRAND 60 65
FT STRAND 69 69

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FT TURN 73 74
 FT STRAND 75 79
 FT TURN 83 85
 FT STRAND 90 94
 FT HELIX 98 105
 FT TURN 106 106
 FT STRAND 109 113
 FT STRAND 116 116
 FT TURN 118 119
 FT STRAND 135 139
 FT STRAND 142 144
 FT TURN 146 147
 FT STRAND 149 149
 FT TURN 151 153
 FT STRAND 156 164
 FT TURN 165 166
 FT STRAND 167 176
 FT STRAND 178 178
 FT STRAND 180 182
 FT HELIX 183 198
 FT STRAND 210 216
 FT TURN 218 219
 FT STRAND 222 226
 FT STRAND 232 232
 FT HELIX 237 241
 FT STRAND 242 246
 FT STRAND 249 251
 FT TURN 252 254
 FT STRAND 256 262
 SQ SEQUENCE 266 AA; 30671 MW; 5ED8A32D11FCA59 CRC64;

Query Match 23.1%; Score 285.5; DB 1; Length 266;
 Best Local Similarity 32.1%; Pred. No. 2.1e-15;
 Matches 75; Conservative 49; Mismatches 91; Indels 19; Gaps 9;

QY 11 DLKXSELRNALSNLROLYYNEKAITENK-ESDDQPLENTLFPKGFTGHPWYNDLLV 69
 DB 37 DLKXSEF-TGTMGNMK--YLYDDHYVSATKYSVDKFLAHLIYINHKKLNNYDKVKT 93
 QY 70 DLGSKDANKYKQKVDLYGAYGYQC-----AGTPNKTCAGYGVTLHDNNRLTEE 122
 DB 94 ELINEDLAKNYDEVVDVYGSNNYVNCYFSSKDNVGVKTGKTCMGJITKEHGNFNDG 153
 QY 123 --KVPINIMIDGKQTVTVIDKVTSKKEVTYQELDLOARHYLHGFGLYNSDSFGKQVQ 180
 DB 154 NLQNVILIRYV-EKKNRTISFE-VQTDKSVTAQELDIKANKFLINKNLYERNSS-SPYE 209
 QY 181 RGLIVHSESGSTVSVDLPDAQOQYPD--TLRIYRDNKNTINSENLHIDLVLVT 232
 DB 210 TGYIKETENNNGNTFWYDMMPAPGDKFDQSKYLMYINDNKTIVDSKSYKIEVHLTT 263

RESULT 72
 006535 PRELIMINARY; PRT; 239 AA.
 AC 006535;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Enterotoxin (Fragment).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=1280;
 RX SEQUENCE FROM N.A.
 RP MEDLINE:94011313; PubMed=8406814;
 RA Mart J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
 RT "Characterization of novel type C staphylococcal enterotoxins:
 biological and evolutionary implications."
 RL Infect. Immun. 61:4254-4262(1993).
 DR EMBL: L13377; AAA2621.1; -.
 DR PDB: 1CKI; X-ray; A=1-239.
 DR GO: GO:0005576; C:extracellular; IEA.

DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bactl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_strep_toxin_1.
 DR Pfam; PF02876; Staph_strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON TER 1
 SQ SEQUENCE 239 AA; 27648 MW; CC3CB3B04E4119E0 CRC64;

Query Match 23.0%; Score 284.5; DB 2; Length 239;
 Best Local Similarity 32.5%; Pred. No. 2.2e-15;
 Matches 76; Conservative 48; Mismatches 91; Indels 19; Gaps 9;

QY 11 DLKXSELRNALSNLROLYYNEKAITENK-ESDDQPLENTLFPKGFTGHPWYNDLLV 69
 DB 10 DLKXSEF-TGTMGNMK--YLYDDHYVSATKYSVDKFLAHLIYINHKKLNNYDKVKT 66
 QY 70 DLGSKDANKYKQKVDLYGAYGYQC-----AGTPNKTCAGYGVTLHDNNRLTEE 122
 DB 67 ELINEDLAKNYDEVVDVYGSNNYVNCYFSSKDNVGVKTGKTCMGJITKEHGNFNDG 126
 QY 123 --KVPINIMIDGKQTVTVIDKVTSKKEVTYQELDLOARHYLHGFGLYNSDSFGKQVQ 180
 DB 127 NLQNVILIRYV-EKKNRTISFE-VQTDKSVTAQELDIKANKFLINKNLYERNSS-SPYE 182
 QY 181 RGLIVHSESGSTVSVDLPDAQOQYPD--TLRIYRDNKNTINSENLHIDLVLVT 232
 DB 183 TGYIKETENNNGNTFWYDMMPAPGDKFDQSKYLMYINDNKTIVDSKSYKIEVHLTT 236

RESULT 73
 005157 PRELIMINARY; PRT; 239 AA.
 AC 005157;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Type C enterotoxin (Fragment).
 OS Staphylococcus intermedius.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=1285;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=95-011195;
 RA Edwards V.M., Deringer J.R., Callantine S.D., Deobald C.F.,
 RL Berger P.H., Kaput V., Stauffacher C.V., Bohach G.A.;
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U91526; AAB50248.1; -.
 DR HSSP; P23313; IJMM.
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bactl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_strep_toxin_1.
 DR Pfam; PF02876; Staph_strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON TER 1
 SQ SEQUENCE 239 AA; 27536 MW; D660644600E4191 CRC64;

Query Match 22.9%; Score 283.5; DB 2; Length 239;
 Best Local Similarity 33.5%; Pred. No. 2.7e-15;
 Matches 79; Conservative 44; Mismatches 90; Indels 23; Gaps 10;

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QY 11 DLRRKSELQARNALSNLRQIY--YNEKAITENK-ESDDQFLENTLLFKGFPTGHPWINDL 67
D 10 DLHKSSEF-TGTMGNMKCLYDDY---VSATKVSVPKFLAHLIDLINISDKLKNYDKV 64
QY 68 LVLDGSDQATNKYRKGVLDLGAAYGYOC-----AGTTPNKACMYGVTLHNNNLT 120
D 65 KTELINEDLAKKYKDEVDVGSNYVNCYSSKDNVKGKVTGKTCMYGGLTKHEGNHFD 124
QY 121 EE--KKVPINIMIDGKQTTVPIDKYKTSKEVTVQELDLQARHYLHKGFLYNSDSPGSK 178
D 125 NGNQNVLIRIY-ENKNTISFD-VQTDKSVTAQELDIKARNFLINKNLYEENS--SP 180
QY 179 VQRLGIYFHSESGSVSYDLFDAGQYPD--TLRIYDNKTINSENHLIDLYLT 232
D 181 YETGYIKFIESNDTWFYDMMPAPGDKFDQSKYLMYSDNKTVDKSVKIEVHLTT 236

RESULT 74
Q8NXJ6 PRELIMINARY; PRT; 266 AA.
ID 08NXJ6
AC 08NXJ6;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE ENTEROTOXIN type C.
GN Name=sec4; OrderedLocuNames=MM0759;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda H., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hirumatsu K.,
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004824; BAB94624.1; -.
DR HSSP; P34071; 1STE.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; BactI_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KM Complete proteome.
SQ SEQUENCE 266 AA; 30670 MW; 4C654659AA48120F CRC64;

Query Match 22.9%; Score 283.5; DB 2; Length 266;
Best Local Similarity 31.1%; Pred. No. 3.1e-15;
Matches 76; Conservative 50; Mismatches 99; Indels 19; Gaps 9;

QY 1 SEKSEINKEKDLRKSELOARNALSNLRQIYYNEKAITENK-ESDDQFLENTLLFKGFPT 59
D 27 AESQPDPTPDELHKSEF-TGTMGNMK--YLYDDHYVSATKVSVDKFLAHLIDLINISDK 83
QY 60 GHPWYNDLLVLDGSDQATNKYRKGVLDLGAAYGYOC-----AGTTPNKACMYGVTL 112
D 84 KLKNYDKVTELINEDLAKKYKDEVDVGSNYVNCYSSKDNVKGKVTGKTCMYGGLT 143
QY 113 LHDNNRLTEE--KKVPINIMIDGKQTTVPIDKYKTSKEVTVQELDLQARHYLHKGFLY 170
D 144 KHEGNHFNPNGNQNVLIRIY-ENKNTISFE-VQTDKSVTAQELDIKARNFLINKNLY 201
QY 171 NSDSFGKQVQRLGIYFHSESGSVSYDLFDAGQYPD--TLRIYDNKTINSENHLIDL 228
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D 202 EFNS--SPYETGYIKFIENNNGNTFWYDMMPAPGDKFDQSKYLMYSDNKTVDKSVKIEV 259
QY 229 YLYT 232
D 260 HLTT 263

RESULT 75
Q06533 PRELIMINARY; PRT; 239 AA.
ID 006533
AC 006533;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Enterotoxin (fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9401313; PubMed=8406814;
RA Marx J.C., Lyon J.D., Roberson J.R., Luppner M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications."
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; U13378; AAA26622.1; -.
DR HSSP; P34071; 1STE.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; BactI_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 239 AA; 27651 MW; A21A954386A8E8625 CRC64;

Query Match 22.8%; Score 282.5; DB 2; Length 239;
Best Local Similarity 31.3%; Pred. No. 3.3e-15;
Matches 76; Conservative 49; Mismatches 99; Indels 19; Gaps 9;

QY 2 EKSEINKEKDLRKSELOARNALSNLRQIYYNEKAITENK-ESDDQFLENTLLFKGFPTG 60
D 1 ESQPDPTPDELHKSEF-TGTMGNMK--YLYDDHYVSATKVSVDKFLAHLIDLINISDK 57
QY 61 HPWYNDLLVLDGSDQATNKYRKGVLDLGAAYGYOC-----AGTTPNKACMYGVTL 113
D 58 LKNYDKVTELINEDLAKKYKDEVDVGSNYVNCYSSKDNVKGKVTGKTCMYGGLTK 117
QY 114 HDNNRLTEE--KKVPINIMIDGKQTTVPIDKYKTSKEVTVQELDLQARHYLHKGFLY 171
D 118 HEGNHFNPNGNQNVLIRIY-ENKNTISFE-VQTDKSVTAQELDIKARNFLINKNLYE 175
QY 172 SDSFGKQVQRLGIYFHSESGSVSYDLFDAGQYPD--TLRIYDNKTINSENHLIDLY 229
D 176 FNS--SPYETGYIKFIENNNGNTFWYDMMPAPGDKFDQSKYLMYSDNKTVDKSVKIEV 233
QY 230 LYT 232
D 234 LTT 236

RESULT 76
FTC2_STAU
ID FTC2_STAU STANDARD; PRT; 266 AA.
AC P34071;
DT 01-FEB-1994 (Rel. 28, Created)
```

DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Enterotoxin type C-2 precursor (SEC2).
 GN Name=entC2;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=1280;
 RN
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
 RA MEDLINE=89277549; PubMed=2543637;
 RX Bohach G.A., Schlievert P.M.;
 RT "Conservation of the biologically active portions of staphylococcal
 RT enterotoxins C1 and C2".
 RL Infect. Immun. 57:2249-2252(1989).
 RN
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RA MEDLINE=96027099; PubMed=7582894; DOI=10.1016/S0969-2126(01)00212-X;
 RX Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua B.F.,
 RA Brehm R.D., Tranter H.S.;
 RT "Crystal structure of the superantigen enterotoxin C2 from
 RT Staphylococcus aureus reveals a zinc-binding site".
 RL Structure 3:769-779(1995).
 RN
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RA MEDLINE=96022987; PubMed=7552730;
 RX Swaminathan S., Furey W.R. Jr., Fletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 RT enterotoxins".
 RL Nat. Struct. Biol. 2:680-686(1995).
 RN
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RA MEDLINE=9734373; PubMed=9191070; DOI=10.1006/jmbi.1997.1023;
 RX Sched E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
 RT "A structural and functional comparison of staphylococcal enterotoxins
 RT A and C2 reveals remarkable similarity and dissimilarity".
 RL J. Mol. Biol. 269:270-280(1997).
 CC
 RT -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication
 RT staphylococcal food poisoning syndrome. The illness characterized
 RT by high fever, hypotension, diarrhea, shock, and in some cases
 RT death.
 CC
 RT -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 RT for the toxin interaction with MHC class II.
 CC
 RT -1- SUBCELLULAR LOCATION: Secreted.
 CC
 RT -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
 RT family.
 CC
 PIR: A60114; A60114.
 DR PDB: 1COV; X-ray; A=28-266.
 DR PDB: 1I4P; X-ray; A=28-266.
 DR PDB: 1I4Q; X-ray; A=28-266.
 DR PDB: 1I4R; X-ray; A=28-266.
 DR PDB: 1I4X; X-ray; A=28-266.
 DR PDB: 1SE2; X-ray; @=28-266.
 DR PDB: 1STE; X-ray; @=28-266.
 DR PDB: 1UNS; X-ray; A=28-266.
 DR InterPro: IPR008992; Bact_endotox.
 DR InterPro: IPR006177; Bactl_tox.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006126; Staph/Strep_tox.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF02876; Staph_strep_tox_C1.
 DR Pfam: PF01123; Staph_strep_toxin; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW 3D-structure: Direct protein sequencing; Enterotoxin, Metal-binding;
 KW Signal; Superantigen; Toxin; Zinc.
 FT SIGNAL 1 27
 FT CHAIN 28 266 Enterotoxin type C-2.
 FT DISULFID 120 137
 FT METAL 36 36 Zinc.
 FT METAL 110 110 Zinc.
 FT METAL 145 145 Zinc.
 FT METAL 149 149 Zinc.

FT HELIX 35 37
 FT HELIX 41 43
 FT STRAND 44 44
 FT TURN 48 48
 FT TURN 49 49
 FT STRAND 50 55
 FT STRAND 59 69
 FT TURN 73 74
 FT TURN 75 79
 FT TURN 83 86
 FT STRAND 90 94
 FT HELIX 98 104
 FT TURN 105 106
 FT STRAND 109 113
 FT STRAND 116 116
 FT TURN 118 119
 FT TURN 128 129
 FT STRAND 136 139
 FT STRAND 142 144
 FT TURN 146 147
 FT STRAND 149 149
 FT HELIX 151 153
 FT STRAND 156 164
 FT TURN 165 166
 FT STRAND 167 176
 FT STRAND 178 178
 FT STRAND 180 182
 FT HELIX 183 198
 FT STRAND 208 216
 FT TURN 218 219
 FT STRAND 222 226
 FT STRAND 232 232
 FT HELIX 237 241
 FT HELIX 242 246
 FT STRAND 249 251
 FT TURN 252 254
 FT STRAND 256 263
 SQ SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;
 Query Match 22.7%; Score 281.5; DB 1; Length 266;
 Best local Similarity 31.1%; Pred. No. 4.5e-15;
 Matches 76; Conservative 50; Mismatches 99; Indels 19; Gaps 9;
 QY 1 SEKSEINERKDKRKSELDQNALNSNRQIYYNKAITENK-ESDDQPLENTLLPFGFF 59
 DB 27 AESQPDPTDELRKSSRP-TGTGNKK--VLYDDHYVATKWSVDKFLAHLILINISDK 83
 QY 60 GHPWYNDLVLDGSKDATTNKKGKVDLYGAYGYOC-----AGTPTKTAQMGYVT 112
 DB 84 KLMYKVKTELLENDLAKKIDVVDYGSNTYNNCFSSKDNVKGKVGKTCMGGIT 143
 QY 113 LHDNNRLTEB--KRVINIMIDGQTTVPIDKYSKEVTVQELDQARHYLHGKFLY 170
 DB 144 KHEGNHFDNGNLDNLIRVY-ENKRNITISPE-VQTDKKSVAQELDIKAPNFIINKNLY 201
 QY 171 NSPSFGKQVQGLIVHSSSGSVSYDLPDAQGYD--TLLEIYDNTKINSENLHIDL 228
 DB 202 EFNSS--SPVETGYIKFIENNGNTFWYDMPAPADKFDQSKYLLMYNDKNTVDSKSVKIEV 259
 QY 229 YLYT 232
 DB 260 HLYT 263
 RESULT 77
 QYX06 PRELIMINARY; PRT; 207 AA.
 AC QYX06; 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Enterotoxin type I (Fragment).
 OS Staphylococcus aureus.

```
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BS49;
RA Blotica G.; Pennacchia C.; Casaburi A.; Ercolini D.; Fusco V.,
RL Villani F.;
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY291446; AAP78528.1; -.
DR HSSP; P13163; 1ESF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_cox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_cox_C; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 207
SQ SEQUENCE 207 AA; 23867 MW; C815DEC021FPA681 CRC64;

Query Match 22.7%; Score 280.5; DB 2; Length 207;
Best Local Similarity 34.7%; Pred. No. 4e-15;
Matches 67; Conservative 32; Mismatches 61; Indels 33; Gaps 7;

QY 23 LSNLRQIY----YNEKAITENKESDDQFLENTLLFKGFPTGHPWYNDLVLDGSKDXTN 78
DB 30 VGNLRNFYTKHDYIDLKGVTDKNLPIANQLF-----FSTG---TNDLISESNWDEIS 79
QY 79 KYKGKVDLYGAYYGQCAAGTGNKTAAGYGVTLHDNNRLTEKKVPIINLMIDKQTTV 138
DB 80 KFKKKDIDFIDIVNPGC-----KSKYMGATL-SCQYNSARKIPINLMVNGKHKT 132
QY 139 PIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFG-GK-----VGKGLIVF 186
DB 133 STDIAINKKAVTFAQELIDYLRRLYLQEEVNYIGHNNTGKGGKYGKSPFYSGFNKKVLF 192
QY 187 HSESGTVSYDLP 199
DB 193 HLNNEKSPSYDLF 205

RESULT 78
Q6XZ6 PRELIMINARY; PRT; 222 AA.
AC Q6XZ6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Enterotoxin seb variant (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=339E;
RA MEDLINE=22943091; PubMed=14580397; DOI=10.1016/S0890-8508(03)00058-6;
RL Lerecure C.; Perelle S.; Dilaeser F.; Fach P.;
RT "A strategy based on 5' nuclease multiplex PCR to detect enterotoxin
RT genes sea to sej of Staphylococcus aureus.";
RL Mol. Cell. Probes 17:227-235(2003).
DR EMBL; AY196689; AAP37186.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; BactI_cox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_cox.
DR InterPro; IPR006173; Staph_cox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_cox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
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DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 222
SQ SEQUENCE 222 AA; 26355 MW; E699C4F9BA858D50 CRC64;

Query Match 22.7%; Score 280.5; DB 2; Length 222;
Best Local Similarity 34.5%; Pred. No. 4.4e-15;
Matches 78; Conservative 42; Mismatches 87; Indels 19; Gaps 8;

QY 11 DLRRKSELQRNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTGHPWYNDLVLD 70
DB 2 ELHAKSKF-TGLMNMKVLVDNHNVSAL-NVKSIDQFLYPLILISIKDTKGNIDNVAVE 59
QY 71 LGSKDANIKYKKKVDLYGAYYGQCAAGTGNKTAAGYGVTLHDNNRLT 120
DB 60 FKNVDLADKYKDKYVDYFGAYYGQCAAGTGNKTAAGYGVTLHDNNRLT 119
QY 121 EEKVPINLMIDGQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVVQ 180
DB 120 KYRSITVAFEDGK-NLISFD-VQTNKKVTAQELDYLTRHYLVKNNKLYEFNN--SPYE 175
QY 181 RGLIVFHSESGTVSYDLPDAQGYPD--TLRLIYRDNKKTINSENL 224
DB 176 TGYIKTFISENS-FWYDMMPAPGDKFDQSKYLMYTNNDKLVDSKDV 220

RESULT 79
Q6ST49 PRELIMINARY; PRT; 239 AA.
AC Q6ST49;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin C2 (Fragment).
GN Name=SEC2;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC Xu M.; Zhang C.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY450554; AAR20496.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; BactI_cox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_cox.
DR InterPro; IPR006173; Staph_cox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_cox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT CHAIN 1
SQ SEQUENCE 239 AA; 27585 MW; 6A7828027F893822 CRC64;

Query Match 22.7%; Score 280.5; DB 2; Length 239;
Best Local Similarity 31.3%; Pred. No. 4.8e-15;
Matches 76; Conservative 49; Mismatches 99; Indels 19; Gaps 9;

QY 2 EKSEINEKDLRKKESELQRNALSNLRQIYYNEKAITENK-ESDDQFLENTLLFKGFPTG 60
DB 1 ESQDPPTPEDELAKSSSF-TGTMGNMK--LYVDHIVSATKVMSSVDKFLAHLIINISDK 57
QY 61 HPWYNDLVLDGSKDANIKYKKKVDLYGAYYGQCAAGTGNKTAAGYGVTL 113
DB 58 LKNDVKVTELLNDLAKKYDEVVDYGSNYVNCYSSKDNVSKVGTGKMGVGGITK 117
QY 114 HDNNRLTEE--KQVPINLMIDGQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYN 171
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Db 118 HEGNHFDNGNLQNVILIRY-ENKNTISFE-VQTDKSVTAQELDIKARNFLINKNLYE 175
Qy 172 SPSFGKVGRLIVHSSGSGTVSYDLFPAQGYPP--TLKRYRNKNTINSENHIDY 229
Db 176 FNS--SPYETGYIKFIENNNGTFWDMMPADGDKFQSKYLMYNDKNTVDSKXIEVH 233
Qy 230 LYT 232
Db 234 LTT 236

RESULT 80
054696 PRELIMINARY; PRT; 236 AA.
ID 054696;
AC 054696;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN Name=spea;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxId=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS156;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Sclander R.K., Musser J.M.;
RT Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes."
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL; X61573; CAA43771.1; -.
DR PIR; S18789; S18789.
DR HSSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal
FT NON_TER 1 1
FT SIGNAL <1 22 Potential.
FT CHAIN 23 >236 type A exotoxin.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27575 MW; 70F54120E79127DF CRC64;

Query Match 22.6%; Score 279.5; DB 2; Length 236;
Best Local Similarity 33.5%; Pred. No. 5.7e-15;
Matches 76; Conservative 4; Mismatches 99; Indels 11; Gaps 7;

Qy 4 SEINKEKDLRKSELDQNAL-SNLRQY--YNEKATEKESDDQPLENTLLFKGFFTG 60
Db 17 SQEVPAQODBNPESQLHRSSLVKNLQNTFLYEGDPVAVHENVKSYVDLLSHDLIN--VS 73
Qy 61 HPWYNDLVDLGSKDATNKKYGGKVDLYGAYYGYOC-AGSTPNKTAQMGYVTLHDNRL 119
Db 74 GLNYVDLKTLELKNREKSTLFGKNQVDLYGVEYYHYCYLGNNAKBRACIYGGVTHNHNH 133
Qy 120 TEKKKYPINIMIGKQTTVPIDKYTKSKKQVTVQELDQARHYLHGKFGLYNSDSFGKY 179
Db 134 EIKKNLIVKYSIDGIQ-SLSFD-IEFSKQVTAQELDYKRYKHLTDNKKQLYTNGP--SKY 189
Qy 180 QRLGIYHSSGSGTVSYDLFPAQGYPP--TLKRYRNKNTINSENHIDY 226
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Db 190 ETGYIKFSKDKETWFDFEPPEPNOVKYLMYXNDNETLDSSTSQI 236
RESULT 81
09F0L6 PRELIMINARY; PRT; 271 AA.
ID 09F0L6;
AC 09F0L6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Staphylococcus enterotoxin C-bovine.
GN Name=sec-bov;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20566668; PubMed=1114901; DOI=10.1128/JB.183.1.63-70.2001;
RA Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RA Meaney W.J., Smyth C.J.;
RT "Characterization of a putative pathogenicity island from bovine
RT Staphylococcus aureus encoding multiple superantigens."
RL J. Bacteriol. 183:63-70(2001).
DR EMBL; AF217235; AAG29599.1; -.
DR HSSP; P34071; 114X.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 271 AA; 31267 MW; 3493F628B042F10 CRC64;

Query Match 22.6%; Score 279.5; DB 2; Length 271;
Best Local Similarity 30.7%; Pred. No. 6.7e-15;
Matches 75; Conservative 53; Mismatches 97; Indels 19; Gaps 9;

Qy 1 SEKSEINKEKDLRKSELDQNAL-SNLRQY--YNEKATEKESDDQPLENTLLFKGFFTG 59
Db 32 ASQGPDPDELDKASKR-TGLMKNKVL--YDQRYVATKYSVDKFLAHLIDLYNISDK 88
Qy 60 GHPWYNDLVDLGSKDATNKKYGGKVDLYGAYYGYOC-----AGSTPNKTAQMGYVTL 112
Db 89 KLNKYDKVTELLNEBLAKKYDEVDVYGSNYYVNCYFSKQNVGKVTGKTCMGGIT 148
Qy 113 LHDNRLTEEK--KVPINIMIGKQTTVPIDKYTKSKKQVTVQELDQARHYLHGKFGLY 170
Db 149 KHEGNHFDNGNLQNVILIRY-ENKNTISFE-VQTDKSVTAQELDIKARNFLINKNLY 206
Qy 171 NDSFGKVGRLIVHSSGSGTVSYDLFPAQGYPP--TLKRYRNKNTINSENHIDY 228
Db 207 EFNS--SPYETGYIKFIENNNGTFWDMMPADGDKFQSKYLMYNDKNTVDSKXIEV 264
Qy 229 LYT 232
Db 265 LTT 268

RESULT 82
P97163 PRELIMINARY; PRT; 236 AA.
ID P97163;
AC P97163;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN Name=spea;
```

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OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCB1_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS165; MGAS327, MGAS493, MGAS494, MGAS167, and MGAS156;
RX MEDLINE=92044323; PubMed=1940804;
RA "Nelson K., Schlivert P.M., Seldner R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes."
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL; X61556; CAA43754.1; -.
DR EMBL; X61555; CAA43753.1; -.
DR EMBL; X61557; CAA43755.1; -.
DR EMBL; X61558; CAA43756.1; -.
DR EMBL; X61559; CAA43757.1; -.
DR EMBL; X61560; CAA43758.1; -.
DR PIR; A60108; A60108.
DR HSSP; P01552; 1SEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bact_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph/Strep_tox.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Signal.
KW NON_TER
FT SIGNAL 1 1 Potential.
FT CHAIN 23 >236 type A exotoxin.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27454 MW; 3FB3F41ABDC13A84 CRC64;

Query Match 22.5%; Score 278.5; DB 2; Length 236;
Best Local Similarity 33.8%; Pred. No. 6.9e-15;
Matches 78; Conservative 43; Mismatches 91; Indels 19; Gaps 10;

OY 4 SEINEKDLRKSEIQRNAL-SNLROIYY-YNEKAIT-ENKESDDQFLNTLLFKGPFVG 60
DB 17 SQEVAQODPPDSQLHRSLSLVKLNQNIYFLYEGDPVTHENVSVQLSHDLIYN---VS 73
OY 61 HPWYNDLLVDLGSKDATNKKYKGVLDYGAYYGOC-AGTPTNKTAQMGVTLHDNNRL 119
DB 74 GPNYDKLKTLELKNQEMATLFDKNDVIYGEVYHLCYLCENARSACTIGVTNHEGNHL 133
OY 120 TEKKVPIINLWIDGQOTVPIDKVTSKKEVTVQELDQARHYLHGKRELVNSDSFGKV 179
DB 134 EIPKTIIVKVSIDGQ-SLSPD-IEFNKKMVAQELDIYVRYLTDNKQLYNGP-SKY 189
OY 180 QRGILVFHSSEGSTVSVDLFD---AQGGYPTLLRIYRDNKNTINSENHIDY 226
DB 190 ETGYIKFIPKNSEFWFDFPEPEFTQSKY----LMIYDNETLDSNLSQI 236

RESULT 83
OY3678 PRELIMINARY; PRT; 239 AA.
ID OY3678;
AC OY3678;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Enterotoxin (Fragment).
OS Streptococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCB1_TaxID=1280;
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; PubMed=8406814;
RA Marx J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications."
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; U13376; AAA26620.1; -.
DR HSSP; P34071; 1I4X.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bact_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph/Strep_tox.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER 1 1
SQ SEQUENCE 239 AA; 27618 MW; A13E7EB25C6989C2 CRC64;

Query Match 22.5%; Score 278.5; DB 2; Length 239;
Best Local Similarity 30.9%; Pred. No. 7e-15;
Matches 75; Conservative 52; Mismatches 97; Indels 19; Gaps 9;

OY 2 EKSEINEKDLRKSEIQRNALSNLROIYYNEKAITENK-ESDDQFLNTLLFKGPFVG 60
DB 1 ESQPDPTDELHKASKF-TGLMENKVL--YDRVSVATKYSVDKFLAHLIYNIISDK 57
OY 61 HPWYNDLLVDLGSKDATNKKYKGVLDYGAYYGOC-----AGTPTNKTAQMGVTL 113
DB 58 LKNYDKVKTLELNEIDLAKKYDEVDYGSNYYNVCYSSKDNQKVTGKTQMGVITK 117
OY 114 HDNRRLTEEK--KVPINLWIDGQOTVPIDKVTSKKEVTVQELDQARHYLHGKFLYN 171
DB 118 HEGNHFNDGKIQNLVIRY-ENKRVLTSE-VQTDKSVTAQELDIKARNPLINKNLYE 175
OY 172 SDSFGKVGQGLIVFHSSEGSTVSVDLFDPAQGYPD--TLRIYRDNKNTINSENHIDY 229
DB 176 FNS--SPETGYIKFIPKNNGTTFWDMIPADQKDFDSKYLMTNIDNKTIVSKYKIEVH 233
OY 230 LYT 232
DB 234 LTT 236

RESULT 84
OY38P4 PRELIMINARY; PRT; 222 AA.
ID OY38P4;
AC OY38P4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Pyrogenic exotoxin A (Fragment).
GN Name=speA;
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCB1_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22508029; PubMed=1620634;
RA Kalia A., Bessen D.E.;
RT "Presence of streptococcal pyrogenic exotoxin A and C genes in human
RT isolates of group G streptococci."
RL FEMS Microbiol. Lett. 219:291-295(2003).
DR EMBL; AY049745; AAL06068.1; -.
DR HSSP; P01552; 1SEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
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DR InterPro: IPR006177; Bcrl1 tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_08.
DR Pfam: PF01123; Staph_strep_toxin; 1.
DR Pfam: PF02876; Staph_strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER 1
FT NON_TER 222
SQ SEQUENCE 222 AA; 25884 MW; 121F8460992818F8 CRC64;

Query Match 22.4%; Score 277.5; DB 2; Length 222;
Best Local Similarity 33.8%; Pred. No. 7.7e-15;
Matches 75; Conservative 41; Mismatches 95; Indels 11; Gaps 7;

QY 4 SEINEKDLRKSELORNAL-SNLROIY--YYNEKAITENKESDDQFLENTLLFKGFTG 60
DB 5 SOEVPFAQDPNPSQLHRSSLVKNLQNIYFLYEGDPVHNENKSVDDLLSHDLIYN--VS 61
QY 61 HPWYNDLVLVDLSKQATNKYKGVLDYGAYYGYOC-AGTPEKTKACMTGGVTLHDNNRL 119
DB 62 GLNYDLKTELKRNREKSTLFFKNQVNDIYGEVEYYHCYLCRNAKRRACIYGVVTHNENHL 121
QY 120 TEKKVPIVLMIDGKQTTVPIDKVKTSKKEVTVQVELDQARHYLHGKFGLYNSDSFGKV 179
DB 122 EIPKNIIVLVNSIDG10-SLSFD-IETSKMVTAGQELDYKVRKGLTDNNQLYTNGP--SKY 177
QY 180 QHGLIVFHSSEGSTVSYDLFDAGQGYPTLLRIYRDNKTINS 221
DB 178 ETGYIKFISKDKETFWDFPPEPFQVQKYLMIYKNETLDS 219

RESULT 85
Q9RSZ4 PRELIMINARY; PRT; 222 AA.
AC Q9RSZ4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Exotoxin type A (Fragment).
GN Name=sgea;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_Taxid=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D633;
RX MEDLINE=99137798; PubMed=9952369;
RA Besen D.E., Izzo M.W., Fiorentino T.R., Caringal R.M.,
RA Hollingshead S.K., Beall B.;
RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
RT tropism in group A streptococci."
RL J. Infect. Dis. 179:627-636(1999).
DR EMBL; AF029051; AAD21315.1; -.
DR HSSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bcrl1 tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_08.
DR Pfam: PF01123; Staph_strep_toxin; 1.
DR Pfam: PF02876; Staph_strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER 1
FT NON_TER 222
SQ SEQUENCE 222 AA; 25884 MW; 121F8460992818F8 CRC64;

```

```

Query Match 22.4%; Score 277.5; DB 2; Length 222;
Best Local Similarity 33.8%; Pred. No. 7.7e-15;
Matches 75; Conservative 41; Mismatches 95; Indels 11; Gaps 7;

QY 4 SEINEKDLRKSELORNAL-SNLROIY--YYNEKAITENKESDDQFLENTLLFKGFTG 60
DB 5 SOEVPFAQDPNPSQLHRSSLVKNLQNIYFLYEGDPVHNENKSVDDLLSHDLIYN--VS 61
QY 61 HPWYNDLVLVDLSKQATNKYKGVLDYGAYYGYOC-AGTPEKTKACMTGGVTLHDNNRL 119
DB 62 GLNYDLKTELKRNREKSTLFFKNQVNDIYGEVEYYHCYLCRNAKRRACIYGVVTHNENHL 121
QY 120 TEKKVPIVLMIDGKQTTVPIDKVKTSKKEVTVQVELDQARHYLHGKFGLYNSDSFGKV 179
DB 122 EIPKNIIVLVNSIDG10-SLSFD-IETSKMVTAGQELDYKVRKGLTDNNQLYTNGP--SKY 177
QY 180 QHGLIVFHSSEGSTVSYDLFDAGQGYPTLLRIYRDNKTINS 221
DB 178 ETGYIKFISKDKETFWDFPPEPFQVQKYLMIYKNETLDS 219

RESULT 86
Q9RSX4 PRELIMINARY; PRT; 234 AA.
AC Q9RSX4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE ENTEROTOXIN=PYROGENIC toxin (Fragment).
OS Staphylococcus.
OC Bacteria; Firmicutes; Bacillales.
OX NCBI_Taxid=1279;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94325995; PubMed=8049778; DOI=10.1006/mpcv.1993.1027;
RA Van den Bussche R.A., Lyon J.D., Bohach G.A.;
RL Mol. Phylogenet. Evol. 2:281-292(1993).
DR HSSP; P34071; I14X.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bcrl1 tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_08.
DR Pfam: PF01123; Staph_strep_toxin; 1.
DR Pfam: PF02876; Staph_strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER 1
FT NON_TER 234
SQ SEQUENCE 234 AA; 27122 MW; D6A7B45FB9810052 CRC64;

Query Match 22.4%; Score 277.5; DB 2; Length 234;
Best Local Similarity 31.6%; Pred. No. 8.2e-15;
Matches 74; Conservative 49; Mismatches 92; Indels 19; Gaps 9;

QY 11 DLARKSELORNALSNLROIYYNEKAITENK-ESDQFLENTLLFKGFTGHPWYNDLVL 69
DB 5 DLHKSSP-TGTGNMK--YLYDNDVVSATKVSVDKFLAHDLIYNSDRLKNYDKVKT 61
QY 70 DLGSKDATNKYKGVLDYGAYYGYOC-----AGTPEKTKACMTGGVTLHDNNRLTEE 122
DB 62 ELNEDLAKKYKDEVVDVGSNYVNCYPSSKDNVGVGTGKTCMTGCGITKHBGNHPDNG 121
QY 123 --KVPINLMIDGKQTTVPIDKVKTSKKEVTVQVELDQARHYLHGKFGLYNSDSFGKVQ 180
DB 122 NLQNVIVRVY-ENKRTITSE-VQTDKSVTAGQELDIKANFLINKNLTFFNS--SPYE 177
QY 181 RGLIVFHSSEGSTVSYDLFDAGQGYPT--TLRIYRDNKTINSENLHIDLYLT 232

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Db 178 TGYIKFIENNNTFWYDMMRPAKGFKDFGDSKYLMMYNNDKRVTDSKSVKLEIVHLTT 231

RESULT 87

054779 PRELIMINARY; PRT; 236 AA.

AC 054779; 054613; 054736; 054740; 054741;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Type A exotoxin precursor (Fragment).

GN Name=apeA;

OS Streptococcus pyogenes.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=1314;

RN [1]

RP SEQUENCE FROM N.A.

RC STPAIN-MGAS485, MGAS158, MGAS491, MGAS495, and MGAS624;

RK MEDLINE=92044323; PubMed=1940804;

RT Nelson K., Schillervert P.M., Selander R.K., Musser J.M.;

RT "Characterization and clonal distribution of four alleles of the speA

RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in

RT Streptococcus pyogenes.";

RL J. Exp. Med. 174:1271-1274(1991).

DR EMBL; X61569; CAA43767.1; -.

DR EMBL; X61568; CAA43766.1; -.

DR EMBL; X61570; CAA43768.1; -.

DR EMBL; X61571; CAA43769.1; -.

DR EMBL; X61572; CAA43770.1; -.

DR PIR; A60108; A60108.

DR HSSP; P01552; 1SEB.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0009405; P:pathogenesis; IEA.

DR InterPro; IPR008992; Bact_endoxo.

DR InterPro; IPR006177; Bactl_tox.

DR InterPro; IPR006123; Scap/Strep_toxin.

DR InterPro; IPR006126; Scaph/Strep_tox.

DR InterPro; IPR006173; Scaph_tox_OB.

DR Pfam; PF01123; Scap_strep_toxin_1.

DR Pfam; PF02876; Scap_strep_tox_C_1.

DR PRINTS; PR00279; BACPRLOXIN

DR PROSITE; PS00277; STRAPH_STREP_TOXIN_1; 1.

DR PROSITE; PS00278; STRAPH_STREP_TOXIN_2; 1.

KW SIGNAL.

FT NON_TER 1 1 potential.

FT SIGNAL <1 22 type A exotoxin.

FT CHAIN 23 >236

FT NON_TER 236 236

SO SEQUENCE 236 AA; 27468 MW; 29DF2AD575623A84 CRC64;

Query Match 22.4%; Score 277.5; DB 2; Length 236;

Best Local Similarity 33.3%; Pred. No. 8.3e-15;

Matches 77; Conservative 44; Mismatches 91; Indels 19; Gaps 10

QY 4 SEBINEDKLRKKSSELOARNL-SNLRIQIYY-YNEKAIT-ENKESDDQFLENTLLFKGPFPG 60

Db 17 SQEYFAQDDPPPSQLHRSSLVNQLNIVFLVEGDVPTHEWVKSVDQLLSHDLYN---VS 73

QY 61 HPWNDDLVDGSKDATTNKYKAKVDLYGATYGYQC-AGGTPNKATACMYGGVTLHDNRRL 119

Db 74 GPNYDKLTKEKIDEMATLTFDKNDIIVGEYHYHLCYENABRSACIYGGVTNHEGNHL 133

QY 120 TEEKKVPINLWIDGQOTVPIIDKYTSKKEVYVQELDQARHYLHGKFGLYNSDSFGGKV 179

Db 134 EIPKKIVKVSIDGQ-SLSPD-ITENKMMYTAQGLDKYKRYLLDINKQQLYNGP-SKY 189

QY 180 QRGILVFSHSEGSIVSYDLFD---AGQGYPTLLRIYRDNKNTINSENLHI 226

Db 190 ETGYIKFIPKKKESFMDFPFPEPEFTQSKY-----LMITKDNMTLDSNTNSQI 236

ID	Q9R931	PRELIMINARY;	PRT;	222 AA.
AC	Q9R931;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Exotoxin A (fragment).			
GN	Name=apeA.			
OS	Streptococcus pyogenes.			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			
OX	NCBI_TaxId=1314;			
RA	[1]			
RA	Sequence from N.A.			
RC	STRAIN=JD709;			
RX	MEDLINE=99137798; PubMed=9952369;			
RA	Bessen D.E., Izzo M.W., Fiorentino T.R., Carling R.M.,			
RA	Hollingshead S.K., Beall B.;			
RT	"Genetic linkage of exotoxin alleles and emm gene markers for tissue			
RT	tropism in group A streptococci."			
RL	J. Infect. Dis. 179:627-636 (1999).			
DR	EMBL; AF055698; AAD11624.1; -.			
DR	PIR; A60108; A60108.			
DR	HSSP; P01552; 1SEB.			
DR	GO; GO:0005576; C:extracellular; IEA.			
DR	GO; GO:0009405; P:pathogenesis; IEA.			
DR	InterPro; IPR008992; Bact_endotox.			
DR	InterPro; IPR006177; Bact1_tox.			
DR	InterPro; IPR006123; Staph/Strep_toxin.			
DR	InterPro; IPR006126; Staph/Strep_tox.			
DR	InterPro; IPR006173; Staph_tox_DB.			
DR	Pfam; PF01123; Staph_Strep_toxin; 1.			
DR	Pfam; PF02876; Staph_Strep_tox_C; 1.			
DR	PRINTS; PR00279; BACTRLTOXIN.			
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.			
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.			
FT	NON_TER	1	1	
FT	NON_TER	222	222	
SQ	SEQUENCE	222 AA;	25759 MW;	488B7ADDCCD91FBA3 CRC64;
	Query Match	22.3%	Score 276.5;	DB 2; Length 222;
	Best Local Similarity	34.1%;	Pred. No. 9.3e-15;	
	Matches	77;	Conservative	43; Mismatches 87; Indels 19; Gaps 10;
QY	4 SEEINERDLKRKSELDQNAL-SNLRLQIYY-YNEKAIT-ENKESDDQLENTLLFKGFFTG 60			
DB	5 SQEYFAQDDPSPQSLHRSLSLVKVLQNTIYFLYEGDPVTHENVKVSVDQLSHDLIYN--VS 61			
QY	61 HPMYNDLLVDIGSDATANKTKGKKVDLYGAIYGYQC-AGSTPNKTLACMYGCVTLHDNNRL 119			
DB	62 GFNYDKLTELKQEMMATLFPDKKVDLYGVEYHLLCYLCENAKRSACIYGGVTNHEGNHL 121			
QY	120 TEEKKVINIMLQSGKOTVPIDKIKTSKKKVTQVQELDQARHYLHGKFGLYNSDPFGKV 179			
DB	122 EIPKTIIVKVSIDIQ-SLSFD-LETNKKVTAQDELVDYKRAKYLTDNKKOLYTNGP--SKY 177			
QY	180 QRGILVHFSSSGSTVSYDLFD---AAGQYPTDLLRIYDNKNTINS 221			
DB	178 ETGYIKFIPIKNKESFMDFPEPEPFQSKY-----LMIYKONETLDS 219			
RESULT	89			
ID	057453	PRELIMINARY;	PRT;	236 AA.
AC	057453;			
DT	01-NOV-1996 (TrEMBLrel. 01, Created)			
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT	05-JUN-2004 (TrEMBLrel. 27, Last annotation update)			
DE	Type A exotoxin precursor (fragment).			
GN	Name=apeA.			
OS	Streptococcus pyogenes.			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			

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OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS156, MGAS250, MGAS256, MGAS285, MGAS480, MGAS492, and
RC MGAS496;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Seldner R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL: X61562; CAA43760.1; -
DR EMBL: X61561; CAA43759.1; -
DR EMBL: X61563; CAA43761.1; -
DR EMBL: X61564; CAA43762.1; -
DR EMBL: X61565; CAA43763.1; -
DR EMBL: X61566; CAA43764.1; -
DR EMBL: X61567; CAA43765.1; -
DR PIR: A60108; A60108.
DR HSSP: P01552; 1SEB.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bactl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006173; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_strep_toxin; 1.
DR Pfam: PF02876; Staph_strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal
FT NON_TER
FT SIGNAL
FT CHAIN
FT NON_TER
SQ SEQUENCE 236 AA; 27484 MW; 2E7F41AAC853600 CRC64;

Query Match 22.0%; Score 272.5; DB 2; Length 236;
Best Local Similarity 33.3%; Pred. No. 2.1e-14;
Matches 77; Conservative 43; Mismatches 92; Indels 19; Gaps 10;

QY 4 SEIRNKDLRKSELOQNL-SNLROYY-YNEKAIT-ENKESDDOFLNTLLFKGFTG 60
DB 17 SQEVFAQODPSPQLHSSLVKNLQNTLYFLYEGDPVTHENVKSYDQLSHDLIYN--VS 73
QY 61 HPWYNDLVLDGSKDATNKYKGVLDYGAAYGYOC-AGGTPNKTAQMGVTLHDNNRL 119
DB 74 GPVYDGLKTELKQWMAITLFDKNVDIYSEYHLCYLGNABRSACITYGVTNHEGNL 133
QY 120 TEEKVPIINIMIDGKQTTVPIDKYTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKV 179
DB 134 EIRKTIIVKVSIGIQ-SLSFP-IEFKKQVTAQELDYKRYKYLTDKQOLYTMGP--SKY 189
QY 180 QRLGIYHSESGSTVSVDLPD---AGQYPTLIRYRNKNTINSENLHI 226
DB 190 ETGYIKFIPKNKSEFWDFPEPFTQSKY---LMIYKQNETLDSNTSQI 236

RESULT 90
ID 006534 PRELIMINARY; PRT; 239 AA.
AC 006534;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=94011313; PubMed=8406814;
RA Marx J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL: U13379; AAA26623.1; -
DR HSSP: F34071; 114X.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bactl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_strep_toxin; 1.
DR Pfam: PF02876; Staph_strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 239 AA; 27517 MW; F354742619C8D196 CRC64;

Query Match 22.0%; Score 272.5; DB 2; Length 239;
Best Local Similarity 30.5%; Pred. No. 2.2e-14;
Matches 74; Conservative 52; Mismatches 98; Indels 19; Gaps 9;

QY 2 EKESEINERDLRKSELOQNL-SNLROYYNEKAITENK-ESDDOFLNTLLFKGFTG 60
DB 1 ESQPDPTPELHKASGF-TGLMNMKVL--YDRIYSAIKVSVDFLHDLIYNSDKK 57
QY 61 HPWYNDLVLDGSKDATNKYKGVLDYGAAYGYOC-----AGTTPNKTAQMGVTL 113
DB 58 LKNYDKVKTIELNEDIAKKYDEVVDVGSNNYVNCFFSSKDNVGVGTGKTCMYGKITK 117
QY 114 HDNNRLTEE--KKVPINIMIDGKQTTVPIDKYTSKKEVTVOELDQARHYLHGKFGLYN 171
DB 118 HEGNHDPDNGNLQVLLRVY-ENKRNITSE-VQTDKSVTAQELDKASFLNKKNLVE 175
QY 172 SDSFGKVORGLIVFSSSGSTVSVDLPDAGQYPD--TLIRYRNKNTINSENLHI 229
DB 176 FNS--SPYETGYIKFLENNGNITWYDMAPGDKFQSKYIMYNNKNTYDSVSLIEVH 233
QY 230 LYT 232
DB 234 LTT 236

RESULT 91
ID 054971 PRELIMINARY; PRT; 260 AA.
AC 054971;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Superantigen.
GN Name=SSA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wellier;
RX MEDLINE=9422556; PubMed=8168951;
RA Reda K.B., Kapur V., Molllick J.A., Lamphear J.G., Musser J.M.,
RA Rich R.R.;
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
RL Infect. Immun. 62:1867-1874(1994).
DR EMBL: U29565; AAA65928.1; -
DR PDB: 1BXT; X-ray; A/B=27-260.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.

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DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006173; Bactrl_tox.
DR InterPro; IPR006126; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph/Strep_tox.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 260 AA; 29757 MW; 2DD96017DE9DAF49 CRC64;

Query Match 21.8%; Score 269.5; DB 2; Length 260;
Best Local Similarity 33.1%; Pred. No. 4.3e-14;
Matches 78; Conservative 37; Mismatches 98; Indels 23; Gaps 9;

QY 5 EINEKDLRKSELDORNLNSLRQIYYNEKAITENKESDDQFLNTLTLFKGFTGHWPY 64
DB 35 EQLN-----SSQFTGVGNLRCL-YDNHFEVETNVASTQQLQHDLIFFPKDLKLNKY 87
QY 65 NDILVDLGSKDATNKKYKGVLDYGAYYGYOCAGTPTN-----KTACWYGGVTLHDNRRL 119
DB 88 DSVKTEFNSKDLATKXKKKVDIFGSNNYYNCYSEGSCKNAKKTCTWYGVTEHHRQI 147
QY 120 TEEKKVPINLMI--DGKQTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFG 176
DB 148 --EGKFP-NITVVKYEDNENILSPD-ITTNKKQVTVQELDCKTRKILVSRKULVEFNN-- 201
QY 177 GKVGRLIVFHSSESTVSYDLFDAGQGYPD--TLRLRYDNKKTINSENLHIDLXL 230
DB 202 SPYETGYIKFTLESSGDSFWYDMPAPGALFDQSKYLMYLNNDKTVSSSAIAIEVHL 257

RESULT 92
ID Q54738 PRELIMINARY; PRT; 260 AA.
AC Q54738;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Superantigen SSA.
GN Name=ssa;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS 1842;
RA MEDLINE=94222556; PubMed=8168951;
RA Reda K.B., Kapur V., Molllick J.A., Lamphear J.G., Musser J.M.,
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
RL Infect. Immun. 62:1867-1874(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS 1842;
RA MEDLINE=96178602; PubMed=8606073;
RA Reda K.B., Kapur V., Goela D., Lamphear J.G., Musser J.M., Rich R.R.;
RT "Phylogenetic distribution of streptococcal superantigen SSA allelic
RT variants provides evidence for horizontal transfer of ssa within
RT Streptococcus pyogenes.";
RL Infect. Immun. 64:1161-1165(1996).
DR EMBL; U48793; AB02149.1; -.
DR HSSP; Q5471; 1BXT.
DR GO; GO:000576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_Strep_tox_C; 1.
DR InterPro; IPR006173; Staph_Strep_tox_C; 1.
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DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 260 AA; 29836 MW; C12215163B42AD6 CRC64;

Query Match 21.6%; Score 267.5; DB 2; Length 260;
Best Local Similarity 33.1%; Pred. No. 6.2e-14;
Matches 78; Conservative 37; Mismatches 98; Indels 23; Gaps 9;

QY 5 EINEKDLRKSELDORNLNSLRQIYYNEKAITENKESDDQFLNTLTLFKGFTGHWPY 64
DB 35 EQLN-----SSQFTGVGNLRCL-YDNHFEVETNVASTQQLQHDLIFFPKDLKLNKY 87
QY 65 NDILVDLGSKDATNKKYKGVLDYGAYYGYOCAGTPTN-----KTACWYGGVTLHDNRRL 119
DB 88 DSVKTEFNSKDLATKXKKKVDIFGSNNYYNCYSEGSCKNAKKTCTWYGVTEHHRQI 147
QY 120 TEEKKVPINLMI--DGKQTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFG 176
DB 148 --EGKFP-NITVVKYEDNENILSPD-ITTNKKQVTVQELDCKTRKILVSRKULVEFNN-- 201
QY 177 GKVGRLIVFHSSESTVSYDLFDAGQGYPD--TLRLRYDNKKTINSENLHIDLXL 230
DB 202 SPYETGYIKFTLESSGDSFWYDMPAPGALFDQSKYLMYLNNDKTVSSSAIAIEVHL 257

RESULT 93
ID Q79X14 PRELIMINARY; PRT; 260 AA.
AC Q79X14;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE SSA.
GN OrderedLocusNames=SPB1119;
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1;
RA MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
RA Okahashi N., Kawabata S., Yamazaki K., Shida T., Yasunaga T.,
RA Hayashi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT large-scale genomic rearrangement in invasive strains and new insights
RT into phage evolution.";
RL Genome Res. 13:1042-1055 (2003).
DR EMBL; AP005144; BAC64214.1; -.
DR GO; GO:000576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 260 AA; 29767 MW; EALFBYCCAE80F99B CRC64;

Query Match 21.6%; Score 267.5; DB 2; Length 260;
Best Local Similarity 33.1%; Pred. No. 6.2e-14;
Matches 78; Conservative 37; Mismatches 98; Indels 23; Gaps 9;

QY 5 EINEKDLRKSELDORNLNSLRQIYYNEKAITENKESDDQFLNTLTLFKGFTGHWPY 64
```

Db 35 EQLN-----KSSQFTGWNKLRCL-YDNHFEVGTNVRSTGQLDHPIDKIDLKXNY 87
Qy 65 NDLDVLDGSKDATNTYKKGKVDLYGAYYICQAGTNP-----KTRACMGVTLTLDNRRL 119
Db 88 DSVKTEFNSKDLAAKYKKNVDIFGNSYNYCYSEGNCSKNAKTCMVGTEHHRNDI 147
Qy 120 TEKKVPIINLWI---DGKQTVPIDVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFG 176
Db 148 --EGKFP-NITVKYVEDNENILSPD-ITTNKQVTVQELDCTRKILVSRKILYERN-- 201
Qy 177 GKVQGLIVFHSSEGSTVSYDLFDAQGYPD--TLIRYRDNKNTINSNLHIDLVL 230
Db 202 SPYENGVIKFISSGDSFWYDWWPAPGALFDQSKYLMYNDKVTSSSAIAIEVHL 257
RESULT 94
ID 054739 PRELIMINARY; PRT; 260 AA.
AC 054739; 054737;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DT 25-OCT-2004 (TREMREL. 28, Last annotation update)
DE Supranantigen SSA.
GN Name=ssa;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS 58;
RX MEDLINE=94222556; PubMed=8168951;
RA Reda K.B., Kapur V., Molllick J.A., Lamphear J.G., Musser J.M.,
RA Rich R.R.;
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal supranantigen gene (ssa) from Streptococcus pyogenes.";
RL Infect. Immun. 62:1867-1874(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS 58;
RX MEDLINE=96178602; PubMed=8606073;
RA Reda K.B., Kapur V., Goela D., Lamphear J.G., Musser J.M., Rich R.R.;
RT "Phylogenetic distribution of streptococcal supranantigen SSA allelic
RT variants provides evidence for horizontal transfer of ssa within
RT Streptococcus pyogenes.";
RL Infect. Immun. 64:1161-1165(1996).
RN EMBL: U48794; AAB02150.1; -;
DR EMBL: U48792; AAB02148.1; -;
DR HSSP: Q54971; IBXT.
DR GO: 0005576; C:extracellular; IEA.
DR GO: 0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bactl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph/Strep_tox.
DR Pfam: PF01123; Staph_Strep_toxin_1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRILTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 260 AA; 29767 MW; EAIFB7CCAB80F99B CRC64;
Query Match 21.6%; Score 267.5; DB 2; Length 260;
Best local Similarity 33.1%; Pred. No. 6.2e-14;
Matches 78; Conservative 37; Mismatches 98; Indels 23; Gaps 9;
Qy 5 EGINEKDLRKSEIQRNALSNLROIYYNEKATENTKESDDQFLNTLLFKFGFTGHPWY 64
Db 35 EQLN-----KSSQFTGWNKLRCL-YDNHFEVGTNVRSTGQLDHPIDKIDLKXNY 87
Qy 65 NDLDVLDGSKDATNTYKKGKVDLYGAYYICQAGTNP-----KTRACMGVTLTLDNRRL 119

Db 88 DSVKTEFNSKDLAAKYKKNVDIFGNSYNYCYSEGNCSKNAKTCMVGTEHHRNDI 147
Qy 120 TEKKVPIINLWI---DGKQTVPIDVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFG 176
Db 148 --EGKFP-NITVKYVEDNENILSPD-ITTNKQVTVQELDCTRKILVSRKILYERN-- 201
Qy 177 GKVQGLIVFHSSEGSTVSYDLFDAQGYPD--TLIRYRDNKNTINSNLHIDLVL 230
Db 202 SPYENGVIKFISSGDSFWYDWWPAPGALFDQSKYLMYNDKVTSSSAIAIEVHL 257
RESULT 95
ID ETC1 STAAU STANDARD; PRT; 266 AA.
AC P01553;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Enterotoxin type C-1 precursor (SEC1).
GN Name=etC1;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88038352; PubMed=2823067;
RA Bohach G.A., Schlievert P.M.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and
RT relatedness to other pyrogenic toxins.";
RL Mol. Gen. Genet. 209:15-20(1987).
RN [2]
RP SEQUENCE OF 28-266.
RX MEDLINE=83213327; PubMed=6189824;
RA Schmidt J.U., Spero L.;
RT "The complete amino acid sequence of staphylococcal enterotoxin C1.";
RL J. Biol. Chem. 258:6300-6306(1983).
CC -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC -----
DR EMBL: X05815; CAA29260.1; -;
DR HSSP: P34071; I14X.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bactl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph/Strep_tox.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR Pfam: PF01123; Staph_Strep_toxin_1.
DR PRINTS: PR00279; BACTRILTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Direct protein sequencing; Enterotoxin; Signal; Supranantigen; Toxin.
FT SIGNAL 1 27
FT CHAIN 28 266 Enterotoxin type C-1.
FT DISULFID 120 137
FT CONFLICT 177 177 D -> N (in Ref. 2).
SQ SEQUENCE 266 AA; 30546 MW; 3A7AB59A896853B CRC64;
Query Match 21.5%; Score 266.5; DB 1; Length 266;

Best Local Similarity 30.5%; Pred. No. 7.7e-14;
Matches 74; Conservative 51; Mismatches 101; Indels 17; Gaps 8;
QY 1 SEKSEINEKDKRKSEIQRNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFTG 60
DB 27 AESQDPFPELHAKSKF-TGLEMNKVLVDHYSAIKYK-SVKFLAHLIDLYISDK 84
QY 61 HPWYNDLLVDLSKDATNKYKGVLDYGAYYGYOC-----AGTPNKACMYGVTL 113
DB 85 LKNDYKVTLELNEGLAKKYKDEVDVYGSNNYVNCYFSSKDNVGMTGKTGMGATK 144
QY 114 HDNRRLTEE--KKVYINMIDGKQTTVPIDKTKSKETVVELDQARHYHGFGLYN 171
DB 145 HEGHNFNDGNLQNVILIRY-ENKRTTISFE-VQTDKSVTAQELDIKANFLINKNLYE 202
QY 172 SDSFGKQVQGLIVFHSSEGSTVSYDLFDAQGYPD--TLIRYRDNKTINSENLHIDY 229
DB 203 FNS--SPETGYIKTEENNGNTFWYDMFAPGDKPDQSKYLMYNDKTVDSKSYKIEVH 260
QY 230 LYT 232
DB 261 LTT 263

RESULT 96
Q6GFN2 PRELIMINARY; PRT; 258 AA.
AC Q6GFN2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin.
GN OrderedLocustNames=SA1916;
OS Staphylococcus aureus (strain MRS252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=282458;
RX [1]
SEQUENCE FROM N.A.
RP PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Baon N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd J., Jagsels K.,
RA James K.D., Lennard M., Line A., Mayes R., Moule S., Mungall K.,
RA Omond D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL: BX571856; CAG40902.1; -.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bactr_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006173; Staph/Strep_toxin.
DR Pfam: PF01123; Staph_strep_toxin_1.
DR Pfam: PF02876; Staph_strep_toxin_C_1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 29855 MW; 722C8517945DDFES CRC64;

Query Match 21.4%; Score 264.5; DB 2; Length 258;
Best Local Similarity 29.5%; Pred. No. 1.1e-13;
Matches 75; Conservative 51; Mismatches 85; Indels 43; Gaps 12;
QY 1 SEKSEINEKDKRKSEIQRN--ALSNLRLQIYY--YNEKAITENKESDDOFLNTLLFK 55
DB 25 SQDPKIDE--LNKSDYKSNKGTGNVNLNLYMSPVEGRGVINSR----QFLSHDLIFP 78

QY 56 GFTGHPYNDLLVDLSKDATNKYKGVLDYGAYYGYOC-----GTPNK 103
DB 79 --IEYKSYNEKVEKTELENTLANNYKGGKVDIFGVPPYPTCTIIPKSEPDINQNFSG---- 131
QY 104 TACWYGVTLLH--DNNRLTEERKVPINLMIDGKQTTVPIDKTKSKETVVELDQARH 161
DB 132 -CMYGGJTFNSSENER--DKLITVQVTLNRSGLG--PITTKNNVTTQELDYKARH 185
QY 162 YLHGFGLYNSDSFGKQVQGLIVFHSSEGSTVSYDLFDAQGYPD--TLIRYRDNKT 218
DB 186 WLTKKKLYEPD--GSAPESGYIKTEKNTSFWFDLPKKELVPFVYKFLNITGDKKV 243
QY 219 INSENLHIDLYLT 232
DB 244 VDSKIKMEVPLNT 257

RESULT 97
Q6ZNF2 PRELIMINARY; PRT; 258 AA.
AC Q6ZNF2;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Enterotoxin type Gv.
GN Name=seg2;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
RX [1]
SEQUENCE FROM N.A.
RP MEDLINE=20260630; PubMed=10803494;
RA Abe J., Ito Y., Onimaru M., Kohsaka T., Takeda T.;
RT "Characterization and distribution of a new enterotoxin-related
RT superantigen produced by Staphylococcus aureus.";
RL Microbiol. Immunol. 44:79-88(2000).
DR EMBL: AB016487; BAA36693.1; -.
DR HSP: P01552; ISEB.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bactr_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006173; Staph/Strep_toxin.
DR Pfam: PF01123; Staph_strep_toxin_1.
DR Pfam: PF02876; Staph_strep_toxin_C_1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 258 AA; 29839 MW; 1229246D83F4FB77 CRC64;

Query Match 21.2%; Score 262.5; DB 2; Length 258;
Best Local Similarity 29.5%; Pred. No. 1.6e-13;
Matches 72; Conservative 49; Mismatches 82; Indels 41; Gaps 11;

QY 11 DIRKSEIQRN--ALSNLRLQIYY--YNEKAITENKESDDOFLNTLLFKGFTGHPYIN 65
DB 33 EINKVSDYKSNKGTGNVNLNLYMSPVEGRGVINSR----QFLSHDLIFP--IEYKSYN 85
QY 66 DLYVDLSKDATNKYKGVLDYGAYYGYOC-----GTPNKACMYGVTL 113
DB 86 EYKTELENTLANNYKGGKVDIFGVPPYPTCTIIPKSEPDINQNFSG----CMYGGJTF 140
QY 114 H--DNNRLTEERKVPINLMIDGKQTTVPIDKTKSKETVVELDQARHYHGFGLYN 171
DB 141 NSSENER--DKLITVQVTLNRSGLG--PITTKNNVTTQELDYKARHWTKEKKLYE 195
QY 172 SDSFGKQVQGLIVFHSSEGSTVSYDLFDAQGYPD--TLIRYRDNKTINSENLHIDY 228
DB 196 FD--GSAPESGYIKTEKNTSFWFDLPKKELVPFVYKFLNITGDKKVVDKSKIMEV 253
QY 229 YLYT 232
DB 254 FLNT 257

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RESULT 98
Q6XZET7 ID Q6XZET7 PRELIMINARY; PRT; 222 AA.
AC Q6XZET7;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin sec variant (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=352E;
RX MEDLINE=22943091; PubMed=14580397; DOI=10.1016/S0890-8508(03)00058-6;
RA Letertre C., Perelle S., Dillasser F., Fach P.;
RT "A strategy based on 5' nuclease multiplex PCR to detect enterotoxin
RT genes sea to seJ of Staphylococcus aureus.";
RL Mol. Cell. Probes 17:227-235(2003).
DR EMBL; A196688; AAP37185.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT TER 222
SQ SEQUENCE 222 AA; 25784 MW; 67A0546FF3CD73B1 CRC64;

Query Match 21.0%; Score 259.5; DB 2; Length 222;
Best Local Similarity 31.0%; Pred. No. 2.3e-13;
Matches 70; Conservative 48; Mismatches 89; Indels 19; Gaps 9;

QY 11 DLRKSELRNALSNLRQIYYNEKAITENK-ESDDQFLFNTLLFKFPGFHPMYNDLIV 69
DB 3 ELHKASKP-TGLMNMKVLT--YDRYVSATKVSVDFTLADHLIYINSDKKLKNYDKVKT 59
QY 70 DLGSKDATNKYKGGKVDLYGAYGYOC-----AGSTPNKTAQMYGGVTLHDNNRLTEK 122
DB 60 ELINELDLAKKYKQEVVDVGSNYVANCYFSSKDNVGVKVTGKTCMVGITKHSGNPHDNG 119
QY 123 K-KVPINIMIDKQTTVPIDKYTKSKEVTVQELDQARHYLHGKFGLYNSDSFGSKVQ 180
DB 120 KLONVILIRVY-ENKRPVITISPE-VQTDKSVTAQELDIKAMFLINKNLVEFNS--SPYE 175
QY 181 RGLIVHSSSEGSTVSYDLFDAGOC--YPTTLRIYRDKNTINSENL 224
DB 176 TGVIKIFENNGNTFWYDMPADPKTEQSKYLMWYINDKNTVDSKSV 221

RESULT 99
Q764P6 ID Q764P6 PRELIMINARY; PRT; 264 AA.
AC Q764P6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin precursor.
OS Name=se-int;
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1285;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=AV8004;
RA Futagawa-Saito K., Suzuki M., Ohsawa M., Ohshima S., Sakurai N.,
RA Ba-Thein W., Fukuyasu T.;
RT "Identification and prevalence of an enterotoxin-related gene, se-int,
RT in Staphylococcus intermedius isolates from dogs and pigeons.";
RL J. Appl. Microbiol. 96:1361-1366(2004).
DR EMBL; AB116378; BAD13763.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1..
KM Signal.
FT CHAIN 1 27 Potential.
FT SIGNAL 28 264
SQ SEQUENCE 264 AA; 30532 MW; 52330A55B4CE0E2F CRC64;

Query Match 20.7%; Score 256.5; DB 2; Length 264;
Best Local Similarity 31.0%; Pred. No. 5.1e-13;
Matches 71; Conservative 39; Mismatches 104; Indels 15; Gaps 6;

QY 12 LKRSKELQNALSNLRQIYYNEKAITE-NKESDDQFLFNTLLFKFPGFHPMYNDLIV 70
DB 38 LHKSEPF-KGLMGVNV--YLDRNPFISESNVSIIDSLADHLIFCTRISEIKIYGLVKT 94
QY 71 LGSKDATNKYKGGKVDLYGAYGYOC-----AGSTPNKTAQMYGGVTLHDNNRLTEK 123
DB 95 FASKELAQKTRNKQVDFGANYVANCYFSGKKEGNEDEGKTCMVGATVYBNHLDNHK 154
QY 124 KVPINIMIDKQTTVPIDKYTKSKEVTVQELDQARHYLHGKFGLYNSDSFGSKVQRL 183
DB 155 SQTIYKVFENSCHITTFELQDKLVTAQELDAKARKFLIDRLNLY--EFKSPYETGY 212
QY 184 IYFHSSEGSTVSYDLFDAGOC--YPTTLRIYRDKNTINSENLHLYL 230
DB 213 IKREINDDKSFYDLMPPGNFNQSKYLTMYSDNKTVESEDIKIVHL 261

RESULT 100
Q9ROO5 ID Q9ROO5 PRELIMINARY; PRT; 209 AA.
AC Q9ROO5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mltogenic exotoxin Z 2 (Fragment).
GN Name=smez-2;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2035;
RX MEDLINE=99093428; PubMed=9874566;
RA Proft T., Mofaet S.L., Berkahn C.J., Fraser J.D.;
RT "Identification and characterization of novel superantigens from
RT Streptococcus pyogenes.";
RL J. Exp. Med. 189:89-102(1999).
DR EMBL; AF086626; AAD52087.1; -.
DR PDB; 1ET6; X-ray; A/B=1-209.
DR PDB; 1EUS; X-ray; A/B=1-209.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.

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